GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: May 30, 2008, 10:13:07 ; Search time 99 Seconds
(without alignments)
6154.036 Million cell updates/sec

Title: US-10-574-297-34
Perfect score: 5178
Sequence: 1 MYLDRFRQCPSSLQIPRSAW.....AAGDRINIPWSFHAGYRYSF 1010

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601879884 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200711:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000:*
4: geneseqp2001:*

4: geneseqp2001:*
5: geneseqp2002:*
6: geneseqp2003a:*
7: geneseqp2003b:*
8: geneseqp2004a:*
9: geneseqp2004b:*
10: geneseqp2005:*
11: geneseqp2006:*
12: geneseqp2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5178	100.0	1010	10	ADZ46880	Adz46880 BASB232 p
2	5109	98.7	998	6	ABU22871	Abu22871 Protein e
3	1462	28.2	271	2	AAW27704	Aaw27704 B. pertus
4	1309	25.3	910	5	AAE16184	Aae16184 Bordetell
5	1307	25.2	910	5	AAE17146	Aae17146 Bordetell
6	1307	25.2	910	10	ADZ46876	Adz46876 BASB232 p
7	1304.5	25.2	915	10	ADZ39252	Adz39252 Pertussis
8	1299.5	25.1	911	2	AAR14320	Aar14320 Pertactin
9	1293.5	25.0	911	5	AAE16183	Aae16183 Bordetell
10	1280	24.7	922	2	AAR25578	Aar25578 Bordetell
11	1280	24.7	922	5	AAE16185	Aae16185 Bordetell
12	1274.5	24.6	911	2	AAR26503	Aar26503 prn prote
13	1238.5	23.9	768	6	ABU23088	Abu23088 Protein e
14	1192.5	23.0	759	10	ADZ46890	Adz46890 BASB232 p
15	1122.5	21.7	515	10	ADZ46892	Adz46892 BASB232 p

15	1122.5	21.7	515	10	ADZ46892	Adz46892 BASB232 p
16	1091.5	21.1	922	2	AAR14321	Aar14321 Pertactin
17	1023	19.8	915	10	ADZ46878	Adz46878 BASB232 p
18	804	15.5	274	2	AAW27708	Aaw27708 B. pertus
19	804	15.5	274	2	AAW27709	Aaw27709 B. parape
20	780	15.1	773	6	ABU41966	Abu41966 Protein e
21	778	15.0	397	10	ADZ46894	Adz46894 BASB232 p
22	761.5	14.7	647	10	ADZ46882	Adz46882 BASB232 p
23	756.5	14.6	712	6	ABU39697	Abu39697 Protein e
24	707.5	13.7	482	10	ADZ46888	Adz46888 BASB232 p
25	664.5	12.8	1569	4	AAG98842	Aag98842 E. coli g
26	664.5	12.8	1569	6	ABU15202	Abu15202 Protein e
27	658.5	12.7	1571	10	AEB91292	Aeb91292 Microbial
28	658.5	12.7	1571	10	AED82060	Aed82060 Hyperimmu
29	658	12.7	1567	10	AED82494	Aed82494 Hyperimmu
30	547	10.6	1606	4	ABG30355	Abg30355 Novel hum
31	543.5	10.5	836	10	AEB91317	Aeb91317 Microbial
32	543.5	10.5	836	10	AED82041	Aed82041 Hyperimmu
33	543.5	10.5	863	10	AED82480	Aed82480 Hyperimmu
34	542.5	10.5	836	6	ABU28689	Abu28689 Protein e
35	539.5	10.4	759	6	ABU49929	Abu49929 Protein e
36	524.5	10.1	955	6	ABU15423	Abu15423 Protein e
37	523.5	10.1	638	6	ABU50354	Abu50354 Protein e
38	522.5	10.1	955	10	AEB91469	Aeb91469 Microbial
39	514.5	9.9	1430	6	ABU50527	Abu50527 Protein e
40	464.5	9.0	599	8	ADR72567	Adr72567 Amino aci
41	464.5	9.0	599	11	AEH12532	Aeh12532 Bordetell
42	464.5	9.0	599	11	AEK91792	Aek91792 Bordetell
43	464.5	9.0	599	11	AEL95088	Ael95088 Bordetell
44	463	8.9	602	8	ADR72565	Adr72565 Amino aci
45	463	8.9	602	11	AEH12530	Aeh12530 Bordetell

ALIGNMENTS

RESULT 1
ADZ46880
ID ADZ46880 standard; protein; 1010 AA.
XX
AC ADZ46880;
XX
DT 15-JUN-2007 (revised)
DT 30-JUN-2005 (first entry)
XX
DE BASB232 polypeptide encoded by Orf17.
XX
KW BASB232; vaccine; bacterial infection; bordetella pertussis infection;
KW antibacterial; BOND_PC; serum resistance protein;
KW serum resistance protein [Bordetella pertussis Tohama I]; brkA; BrkA;
KW GO7155.
XX
OS Bordetella pertussis.
XX
PN WO2005032584-A2.
XX
PD 14-APR-2005.
XX
PF 01-OCT-2004; 2004WO-EP011082.
XX
PR 02-OCT-2003; 2003GB-00023112.
PR 02-OCT-2003; 2003GB-00023113.
XX
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
XX
PI Castado C, Denoel P, Godfroid F, Poolman J;
XX

XX
DR WPI; 2005-296056/30.
DR N-PSDB; ADZ46879.
DR PC:NCBI; gi562026.
XX
PT Immunogenic composition, comprises polypeptide of Bordetella pertussis or
PT mixture of different B.pertussis, antigens, useful in Bordetella disease
PT treatments.
XX
PS Claim 3; SEQ ID NO 34; 172pp; English.
XX
CC The invention relates to BASB232 polypeptides (SEQ Group 2), and the
CC polynucleotide sequences (SEQ Group 1) encoding them. The invention also
CC relates to an immunogenic composition, comprising a B. pertussis BASB232
CC polypeptide or a mixture of 2-9 or 10 different B. pertussis antigens,
CC chosen from Bordetella autotransporter protein, Bordetella iron
CC acquisition protein, Bordetella lipoprotein, Bordetella adhesin and
CC Bordetella toxin/invasin, and an excipient. Also described is a vaccine
CC comprising the above immunogenic composition. The immunogenic composition
CC is useful in the preparation of a medicament for use in the treatment or
CC prevention of Bordetella disease such as whooping cough. The immunogenic
CC composition and vaccine are useful for treating or preventing Bordetella
CC infections such as B. pertussis, B. parapertussis or B. bronchiseptica
CC infections, by administering the vaccine to a host. This sequence
CC represents a BASB232 polypeptide of the invention.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 1010 AA;

Query Match 100.0%; Score 5178; DB 10; Length 1010;
Best Local Similarity 100.0%; Pred. No. 2.6e-299;
Matches 1010; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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  Matches 1010;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MYLDRFRQCPSSLQIPRSAWRLHALAAALALAGMARLAPAAAQAPQPPVAGAPHAQDAGQ 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MYLDRFRQCPSSLQIPRSAWRLHALAAALALAGMARLAPAAAQAPQPPVAGAPHAQDAGQ 60

Qy         61 EGEFDHRDNTLIAVFDDGVGINLDDDPDELGETAPPTLKDIHISVEHKNPMSKPAIGVRV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EGEFDHRDNTLIAVFDDGVGINLDDDPDELGETAPPTLKDIHISVEHKNPMSKPAIGVRV 120

Qy        121 SGAGRALTLAGSTIDATEGGIPAVVRRGGTLELDGVTVAGGEGMEPMTVSDAGSRLSVRG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGAGRALTLAGSTIDATEGGIPAVVRRGGTLELDGVTVAGGEGMEPMTVSDAGSRLSVRG 180

Qy        181 GVLGGEAPGVGLVRAAQGGQASIIDATLQSILGPALIADGGSISVAGGSIDMDMGPGFPP 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GVLGGEAPGVGLVRAAQGGQASIIDATLQSILGPALIADGGSISVAGGSIDMDMGPGFPP 240

Qy        241 PPPPLPGAPLAAHPPLDRVAAVHAGQDGKVTLREVALRAHGPQATGVYAYMPGSEITLQG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PPPPLPGAPLAAHPPLDRVAAVHAGQDGKVTLREVALRAHGPQATGVYAYMPGSEITLQG 300

Qy        301 GTVSVQGDDGAGVVAGAGLLDALPPGGTVRLDGTTVSTDGANTDAVLVRGDAARAEVVNT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTVSVQGDDGAGVVAGAGLLDALPPGGTVRLDGTTVSTDGANTDAVLVRGDAARAEVVNT 360

Qy        361 VLRTAKSLAAGVSAQHGGRVTLRQTRIETAGAGAEGISVLGFEPQSGSGPASVDMQGGSI 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VLRTAKSLAAGVSAQHGGRVTLRQTRIETAGAGAEGISVLGFEPQSGSGPASVDMQGGSI 420

Qy        421 TTTGNRAAGIALTHGSARLEGVAVRAEGSGSSAAQLANGTLVVSAGSLASAQSGAISVTD 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTTGNRAAGIALTHGSARLEGVAVRAEGSGSSAAQLANGTLVVSAGSLASAQSGAISVTD 480
```


Qy 481 TPLKLMPGALASSTVSVRLTDGATAQGGNGVFLQQHSTIPVAVALESGALARGDIVADGN 540
Db 481 TPLKLMPGALASSTVSVRLTDGATAQGGNGVFLQQHSTIPVAVALESGALARGDIVADGN 540
Qy 541 KPLDAGISLSVASGAAWHGATQVLQSATLGKGGTWVVNADSRVQDMSMRGGRVEFQAPAP 600
Db 541 KPLDAGISLSVASGAAWHGATQVLQSATLGKGGTWVVNADSRVQDMSMRGGRVEFQAPAP 600
Qy 601 EASYKTLTLQTLDGNGVFVLNTNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARL 660
Db 601 EASYKTLTLQTLDGNGVFVLNTNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARL 660
Qy 661 GLVHTQGQGNATFRLANVGKAVDLGTWRYSLAEDPKTHVWSLQRAGQALSGAANAAVNAA 720
Db 661 GLVHTQGQGNATFRLANVGKAVDLGTWRYSLAEDPKTHVWSLQRAGQALSGAANAAVNAA 720
Qy 721 DLSSIALAESNALDKRLGELRLRADAGGPWARTFSERQQISNRHARAYDQTVSGLEIGLD 780
Db 721 DLSSIALAESNALDKRLGELRLRADAGGPWARTFSERQQISNRHARAYDQTVSGLEIGLD 780
Qy 781 RGWSASGGRWYAGGLLGYTYADRTYPGDGGGKVKGLHVGGYAAYVGDGGYYLDTVLRLGR 840
Db 781 RGWSASGGRWYAGGLLGYTYADRTYPGDGGGKVKGLHVGGYAAYVGDGGYYLDTVLRLGR 840
Qy 841 YDQQYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQAEVMLWRTSGKRYRA 900
Db 841 YDQQYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQAEVMLWRTSGKRYRA 900
Qy 901 SNGLRVKVDANTATLGRLGLRFGRRIALAGGNIVQPYARLGWTQEFKSTGDVRTNGIGHA 960
Db 901 SNGLRVKVDANTATLGRLGLRFGRRIALAGGNIVQPYARLGWTQEFKSTGDVRTNGIGHA 960

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Qy        961 GAGRHGRVELGAGVDAALGKGHNLYASYEYAAGDRINIPWSFHAGYRYSF 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGRHGRVELGAGVDAALGKGHNLYASYEYAAGDRINIPWSFHAGYRYSF 1010


RESULT 2
ABU22871
ID   ABU22871 standard; protein; 998 AA.
XX
AC   ABU22871;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Protein encoded by Prokaryotic essential gene #8398.
XX
KW   Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS   Bordetella pertussis.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L, Zamudio C, Malone C, Hasselbach P, Ohlsen KL, Zweigle TW;
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PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA26741.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 50795; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for

CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 998 AA;

Query Match 98.7%; Score 5109; DB 6; Length 998;
Best Local Similarity 99.9%; Pred. No. 3.3e-295;
Matches 997; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy         13 LQIPRSAWRLHALAAALALAGMARLAPAAAQAPQPPVAGAPHAQDAGQEGEFDHRDNTLI 72
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQIPRSAWRLHALAAALALAGMARLAPAAAQAPQPPVAGAPHAQDAGQEGEFDHRDNTLI 60

Qy         73 AVFDDGVGINLDDDPDELGETAPPTLKDIHISVEHKNPMSKPAIGVRVSGAGRALTLAGS 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AVFDDGVGINLDDDPDELGETAPPTLKDIHISVEHKNPMSKPAIGVRVSGAGRALTLAGS 120

Qy        133 TIDATEGGIPAVVRRGGTLELDGVTVAGGEGMEPMTVSDAGSRLSVRGGVLGGEAPGVGL 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TIDATEGGIPAVVRRGGTLELDGVTVAGGEGMEPMTVSDAGSRLSVRGGVLGGEAPGVGL 180

Qy        193 VRAAQGGQASIIDATLQSILGPALIADGGSISVAGGSIDMDMGPGFPPPPPPLPGAPLAA 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VRAAQGGQASIIDATLQSILGPALIADGGSISVAGGSIDMDMGPGFPPPPPPLPGAPLAA 240

Qy        253 VDPLDPVAAVHAGQDGKVTLDEVALRAHGDQATGVKAVMDGSELTLQGGTVSVGGDGAG 312
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Qy        253 HPPLDRVAAVHAGQDGKVTLREVALRAHGPQATGVYAYMPGSEITLQGGTVSVQGDDGAG 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 HPPLDRVAAVHAGQDGKVTLREVALRAHGPQATGVYAYMPGSEITLQGGTVSVQGDDGAG 300

Qy        313 VVAGAGLLDALPPGGTVRLDGTTVSTDGANTDAVLVRGDAARAEVVNTVLRTAKSLAAGV 372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VVAGAGLLDALPPGGTVRLDGTTVSTDGANTDAVLVRGDAARAEVVNTVLRTAKSLAAGV 360

Qy        373 SAQHGGRVTLRQTRIETAGAGAEGISVLGFEPQSGSGPASVDMQGGSITTTGNRAAGIAL 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SAQHGGRVTLRQTRIETAGAGAEGISVLGFEPQSGSGPASVDMQGGSITTTGNRAAGIAL 420

Qy        433 THGSARLEGVAVRAEGSGSSAAQLANGTLVVSAGSLASAQSGAISVTDTPLKLMPGALAS 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 THGSARLEGVAVRAEGSGSSAAQLANGTLVVSAGSLASAQSGAISVTDTPLKLMPGALAS 480

Qy        493 STVSVRLTDGATAQGGNGVFLQQHSTIPVAVALESGALARGDIVADGNKPLDAGISLSVA 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 STVSVRLTDGATAQGGNGVFLQQHSTIPVAVALESGALARGDIVADGNKPLDAGISLSVA 540

Qy        553 SGAAWHGATQVLQSATLGKGGTWVVNADSRVQDMSMRGGRVEFQAPAPEASYKTLTLQTL 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 SGAAWHGATQVLQSATLGKGGTWVVNADSRVQDMSMRGGRVEFQAPAPEASYKTLTLQTL 600

Qy        613 DGNGVFVLNTNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTQGQGNAT 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 DGNGVFVLNTNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTQGQGNAT 660

Qy        673 FRLANVGKAVDLGTWRYSLAEDPKTHVWSLQRAGQALSGAANAAVNAADLSSIALAESNA 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 FRLANVGKAVDLGTWRYSLAEDPKTHVWSLQRAGQALSGAANAAVNAADLSSIALAESNA 720

Qy        733 LDKRLGELRLRADAGGPWARTFSERQQISNRHARAYDQTVSGLEIGLDRGWSASGGRWYA 792
              ''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 LDKRLGELRLRADAGGPWARTFSERQQISNRHARAYDQTVSGLEIGLDRGWSASGGRWYA 780

Qy        793 GGLLGYTYADRTYPGDGGGKVKGLHVGGYAAYVGDGGYYLDTVLRLGRYDQQYNIAGTDG 852
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGLLGYTYADRTYPGDGGGKVKGLHVGGYAAYVGDGGYYLDTVLRLGRYDQQYNIAGTDG 840

Qy        853 GRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQAEVMLWRTSGKRYRASNGLRVKVDANT 912
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQAEVMLWRTSGKRYRASNGLRVKVDANT 900

Qy        913 ATLGRLGLRFGRRIALAGGNIVQPYARLGWTQEFKSTGDVRTNGIGHAGAGRHGRVELGA 972
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATLGRLGLRFGRRIALAGGNIVQPYARLGWTQEFKSTGDVRTNGIGHAGAGRHGRVELGA 960

Qy        973 GVDAALGKGHNLYASYEYAAGDRINIPWSFHAGYRYSF 1010
                    ||||||||||||||||||||||||||||||||||||
Db        961 GVDAALGKGHNLYASYEYAAGDRINIPWSFHAGYRYSF 998


RESULT 3
AAW27704
ID   AAW27704 standard; protein; 271 AA.
XX
AC   AAW27704;
XX
DT   08-MAY-1998  (first entry)
XX
DE   B. pertussis BrkA protein autotransporter membrane integration region.
XX
KW   BrkA; autotransporter; Gram-negative bacteria; diagnostic; therapy;
KW   surface presented polypeptide.
XX
OS   Bordetella pertussis
```

OS Bordetella pertussis.
XX
PN WO9735022-A1.
XX
PD 25-SEP-1997.
XX
PF 15-MAR-1996; 96WO-EP001130.
XX
PR 15-MAR-1996; 96WO-EP001130.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Maurer J, Jose J, Meyer TF;
XX
DR WPI; 1997-480227/44.
DR N-PSDB; AAT88141.
XX
PT Presentation of peptide(s) on surface of Gram-negative bacteria - via
PT transformation with vector encoding signal peptide, presented peptide and
PT transporter domain of auto-transporter, producing peptide libraries for
PT epitope mapping.
XX
PS Claim 8; Fig 8; 84pp; German.
XX
CC This sequence represents the Bordetella pertussis BrkA autotransporter
CC membrane integration region. This region is involved in a novel method
CC which allows the presentation of stable fusion polypeptides on the
CC surface of Gram-negative bacteria which can be released into the
CC surrounding media. The method can be used to produce a variegated
CC population of surface-presented polypeptides, so that bacteria expressing
CC polypeptides with particular properties can be identified and
CC simultaneously selected, e.g. for epitope mapping or selection of ligands
CC with the highest affinity for antibodies, major histocompatibility
CC complex (MHC) molecules or other components of the immune system

```
CC   complex (MHC) molecules or other components of the immune system.
CC   Selected polypeptides can be used diagnostically, e.g. to screen sera or
CC   antibody banks, and (poly)peptide expressing cells may be used as live
CC   vaccines. They may also be used therapeutically, e.g. when the
CC   polypeptide is an antibody, to remove or concentrate pollutants,
CC   inactivate toxins, prepare and process food, prepare washing compositions
CC   and label cells. Selected bacteria can be stored, reproduced and
CC   replicated on a large scale as individual clones
XX
SQ   Sequence 271 AA;

  Query Match             28.2%;  Score 1462;  DB 2;  Length 271;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-79;
  Matches  271;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        740 LRLRADAGGPWARTFSERQQISNRHARAYDQTVSGLEIGLDRGWSASGGRWYAGGLLGYT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LRLRADAGGPWARTFSERQQISNRHARAYDQTVSGLEIGLDRGWSASGGRWYAGGLLGYT 60

Qy        800 YADRTYPGDGGGKVKGLHVGGYAAYVGDGGYYLDTVLRLGRYDQQYNIAGTDGGRVTADY 859
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YADRTYPGDGGGKVKGLHVGGYAAYVGDGGYYLDTVLRLGRYDQQYNIAGTDGGRVTADY 120

Qy        860 RTSGAAWSLEGGRRFELPNDWFAEPQAEVMLWRTSGKRYRASNGLRVKVDANTATLGRLG 919
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RTSGAAWSLEGGRRFELPNDWFAEPQAEVMLWRTSGKRYRASNGLRVKVDANTATLGRLG 180

Qy        920 LRFGRRIALAGGNIVQPYARLGWTQEFKSTGDVRTNGIGHAGAGRHGRVELGAGVDAALG 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LRFGRRIALAGGNIVQPYARLGWTQEFKSTGDVRTNGIGHAGAGRHGRVELGAGVDAALG 240

Qy        980 KGHNLYASYEYAAGDRINIPWSFHAGYRYSF 1010
              ||||||||||||||||||||||||||||||||
Db        241 KGHNLYASYEYAAGDRINIPWSFHAGYRYSF 271
```

```
Db        241 KGHNLYASYEYAAGDRINIPWSFHAGYRYSF 271


RESULT 4
AAE16184
ID   AAE16184 standard; protein; 910 AA.
XX
AC   AAE16184;
XX
DT   15-JUN-2007  (revised)
DT   26-MAR-2002  (first entry)
XX
DE   Bordetella pertussis pertactin outer membrane protein, p.69.
XX
KW   Pertactin; PRN: outer membrane protein; vaccine; Bordetella infection;
KW   therapy; antibiotic; antibacterial; p.69; BOND_PC; pertactin;
KW   pertactin [Bordetella pertussis]; GO5524; GO7155; GO9405.
XX
OS   Bordetella pertussis.
XX
FH   Key             Location/Qualifiers
FT   Region          254. .309
FT                   /note= "Pertactin region I"
FT   Region          568. .609
FT                   /note= "Pertactin region II"
XX
PN   WO200190143-A2.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-EP006457.
XX
PR   25-MAY-2000; 2000US-0206969P.
XX
```

XX

PA (INSP) INST PASTEUR.

XX

PI Guiso-Maclouf N, Boursaux-Eude C;

XX

DR WPI; 2002-097639/13.

DR N-PSDB; AAD26441.

DR PC:NCBI; gi4572563.

XX

PT Polypeptides containing polymorphisms of the repeated regions of
PT pertactin in Bordetella species, useful in immunogenic compositions for
PT treating infections caused by Bordetella and in diagnostic methods.

XX

PS Disclosure; Page 31; 47pp; English.

XX

CC The present invention relates to Bordetella bronchiseptica pertactin
CC (outer membrane protein) or their fragments. Pertactin (PRN) is used as
CC vaccine. Pertactin antibody is useful for treating Bordetella infections
CC and used to detect Bordetella antigens in biological preparations or in
CC purifying corresponding proteins, glycoproteins or their mixtures when
CC used in affinity chromatographic columns. Pertactin is useful as antigens
CC to identify antibodies to Bordetella in materials such as human or other
CC animal tissue and human or other animal cells, as well as biological
CC fluids, such as human or other animal body fluids, including human sera,
CC and to determine the concentration of Ab in those materials. Thus the
CC antigens can be used for qualitative or quantitative determination of
CC Bordetella in a material. The present sequence is B. pertussis pertactin
CC outer membrane protein, p.69

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX

SQ Sequence 910 AA;

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  Query Match             25.3%;  Score 1309;  DB 5;  Length 910;
  Best Local Similarity   36.7%;  Pred. No. 3.6e-69;
  Matches  332;  Conservative  112;  Mismatches  299;  Indels  162;  Gaps   22;

Qy        247 GAPLAAHPPLDRVAAVHAGQ------------DGKVTLREVALRAHGPQATGVYAYMPGS 294
              ||  |||   :  : |  |:             |  |     ::  | || |:    | :
Db         27 GAAPAAHADWNNQSIVKTGERQHGIHIQGSDPGGVRTASGTTIKVSGRQAQGILLENPAA 86

Qy        295 EITLQGGTVSVQG---DDGAGVVAGAGLLDALPPGGTVRLDGTTVSTDGANTD----AVL 347
              |:  : |:|:  |   |||     |   : |    | :  |  |::  |   |    |:
Db         87 ELQFRNGSVTSSGQLSDDGIRRFLGTVTVKA----GKLVADHATLANVGDTWDDDGIALY 142

Qy        348 VRGDAARAEVVNTVLRTAKSLAAGVSAQHGGRVTLRQTRIETAGAGAEGISVLGFE---- 403
              | |: |:| : :: |:     | ||  : |  ||:::: |   |     :  |  |
Db        143 VAGEQAQASIADSTLQG----AGGVQIERGANVTVQRSAIVDGGLHIGALQSLQPEDLPP 198

Qy        404 -------------PQSGSGPASVDMQGGSITT------TGNRAAGIALTHGS-ARLEGVA 443
                          | ||: ||:| : | |  |       || ||||:|   |:   |:
Db        199 SRVVLRDTNVTAVPASGA-PAAVSVLGASELTLDGGHITGGRAAGVAAMQGAVVHLQRAT 257

Qy        444 VR-------------------------------------AEGSGSS------------- 452
              :|                                     : ||||
Db        258 IRRGDAPAGGAVPGGAVPGGAVPGGFGPGGFGPVLDGWYGVDVSGSSVELAQSIVEAPEL 317

Qy        453 --AAQLANGTLVVSAGSLASAQSGAISVTDTPLKLMPGALASSTVSVRLTDGATAQGGNG 510
                | ::  |  |  :|   ||  | :  |    :  | |   : :|: |  || |||
Db        318 GAAIRVGRGARVTVSGGSLSAPHGNVIETGGARRFAPQA---APLSITLQAGAHAQG--K 372

Qy        511 VFLQQHSTIPVAVALESGALARGDIVA------DGNK--PLDAGISLSVASGAAWHGATQ 562
                | :    || : |  || |:|||||       |    |||    :::|| | | |||:
Db        373 ALLYRVLPEPVKLTLTGGADAQGDIVATELPSIPGTSIGPLD----VALASQARWTGATR 428

Qy        563 VLQSATLGKGGTWVNADSRVQDMSMDG-GDVTFQADADFAAYKTLTLQTLDGNGVTVLN 621
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Qy        563 VLQSATLGKGGTWVVNADSRVQDMSMRG-GRVEFQAPAPEASYKTLTLQTLDGNGVFVLN 621
              : | ::    |||:  :| |  : :   | |:|| ||    :| ||: || |:|:| :|
Db        429 AVDSLSI-DNATWVMTDNSNVGALRLASDGSVDFQQPAEAGRFKVLTVNTLAGSGLFRMN 487

Qy        622 TNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTQGQGNATFRLANVGKA 681
                  | :|:| |   | ||||: |||:| |  |    | || |     ||| |||
Db        488 VFADLGLSDKLVVMQDASGQHRLWVRNSGSEPASANTLL-LVQTPRGSAATFTLANKDGK 546

Qy        682 VDLGTWRYSLAEDPKTHVWSL----------------------------------QRAGQA 708
              ||:||:|| || :     |||                                    ||:
Db        547 VDIGTYRYRLAANGNGQ-WSLVGAKAPPAPKPAPQPGPQPPQPPQPQPEAPAPQPPAGRE 605

Qy        709 LSGAANAAVNAADL---SSIALAESNALDKRLGELRLRADAGGPWARTFSERQQISNRHA 765
              || |||||||   :   |::  |||||| ||||||||  |||| | | |::|||: ||
Db        606 LSAAANAAVNTGGVGLASTLWYAESNALSKRLGELRLNPDAGGAWGRGFAQRQQLDNRAG 665

Qy        766 RAYDQTVSGLEIGLDRGWSASGGRWYAGGLLGYTYADRTYPGDGGGKVKGLHVGGYAAYV 825
              | :|| |:| |:| |   : :||||: ||| |||  || : |||||    :|||||| |:
Db        666 RRFDQKVAGFELGADHAVAVAGGRWHLGGLAGYTRGDRGFTGDGGGHTDSVHVGGYATYI 725

Qy        826 GDGGYYLDTVLRLGRYDQQYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQ 885
               | |:|||  ||  | :  : :||:||  |   ||| |   ||| ||||   : || |||
Db        726 ADSGFYLDATLRASRLENDFKVAGSDGYAVKGKYRTHGVGASLEAGRRFTHADGWFLEPQ 785

Qy        886 AEVMLWRTSGKRYRASNGLRVKVDANTATLGRLGLRFGRRIALAGGNIVQPYARLGWTQE 945
              ||: ::|  |  |||:|||||: :  :: |||||  |:|| |||  |||| :    ||
Db        786 AELAVFRAGGGAYRAANGLRVRDEGGSSVLGRLGLEVGKRIELAGGRQVQPYIKASVLQE 845

Qy        946 FKSTGDVRTNGIGHAGAGRHGRVELGAGVDAALGKGHNLYASYEYAAGDRINIPWSFHAG 1005
              |   | | |||| |    |  | ||| |: ||||:||:|||||||: | :: :||:||||
Db        846 FDGAGTVHTNGIAHRTELRGTRAELGLGMAAALGRGHSLYASYEYSKGPKLAMPWTFHAG 905

Qy       1006 YRYSF 1010
              '''''
```

```
              ||||:
Db        906 YRYSW 910


RESULT 5
AAE17146
ID   AAE17146 standard; protein; 910 AA.
XX
AC   AAE17146;
XX
DT   15-JUN-2007  (revised)
DT   18-APR-2002  (first entry)
XX
DE   Bordetella pertussis pertactin (Prn1) protein.
XX
KW   Pertactin; prn1; antibacterial; immunostimulant; antimicrobial; vaccine;
KW   diphtheria; tetanus; polio; Haemophilus influenza b infection; therapy;
KW   immune response; BOND_PC; pertactin precursor;
KW   pertactin precursor [Bordetella pertussis Tohama I]; prn;
KW   pertactin outer membrane protein;
KW   pertactin outer membrane protein [Bordetella pertussis]; Pertactin;
KW   Pertactin [Bordetella pertussis]; P.69A protein;
KW   P.69A protein [Bordetella pertussis]; GO5515; GO7155; GO9405; GO16020;
KW   GO19867.
XX
OS   Bordetella pertussis.
XX
FH   Key             Location/Qualifiers
FT   Region          597. .604
FT                   /note= "Conserved region"
XX
PN   WO200200695-A2.
XX
PD   03-JAN-2002
```

PD 03-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-NL000493.
XX
PR 30-JUN-2000; 2000EP-00202309.
XX
PA (NEWE-) NEDERLANDEN MIN WELZIJN.
XX
PI Mooi FR;
XX
DR WPI; 2002-139897/18.
DR PC:NCBI; gi464364.
DR PC:SWISSPROT; P14283.
DR PC:BIND; 330939,330940.
XX
PT New polypeptides derived from Bordetella pertussis pertactin, useful as a
PT vaccine against infections caused by Bordetella strains, and other
PT infectious diseases of mammals, e.g. diphtheria, tetanus, or polio.
XX
PS Claim 11; Page 35-38; 52pp; English.
XX
CC The invention relates to polypeptides derived from Bordetella pertussis
CC pertactin (Prn1). The polypeptide is useful in the preparation of
CC vaccines against B. pertussis, B. parapertussis, B. bronchiseptica and
CC other infectious diseases of mammals including diphtheria, tetanus, polio
CC and infections caused by Haemophilus influenza b. The polypeptide is
CC especially useful for eliciting an immune response against Bordetella sp.
CC Antibodies against the polypeptide may be used for pharmaceutical and/or
CC diagnostic purposes, particularly for treating or preventing infections
CC caused by Bordetella pertussis or Bordetella parapertussis. The present
CC sequence is B. pertussis prn1 protein
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

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CC   information from BOND.
XX
SQ   Sequence 910 AA;

  Query Match             25.2%;  Score 1307;  DB 5;  Length 910;
  Best Local Similarity   36.7%;  Pred. No. 4.8e-69;
  Matches  332;  Conservative  112;  Mismatches  299;  Indels  162;  Gaps   22;

Qy        247 GAPLAAHPPLDRVAAVHAGQ------------DGKVTLREVALRAHGPQATGVYAYMPGS 294
              ||  |||   :  : |  |:             |  |     ::  | || |:    | :
Db         27 GAAPAAHADWNNQSIVKTGERQHGIHIQGSDPGGVRTASGTTIKVSGRQAQGILLENPAA 86

Qy        295 EITLQGGTVSVQG---DDGAGVVAGAGLLDALPPGGTVRLDGTTVSTDGANTD----AVL 347
              |:  : |:|:  |   |||      |   : |    | :  |  |::  |   |    |:
Db         87 ELQFRNGSVTSSGQLSDDGIRRFLGTVTVKA----GKLVADHATLANVGDTWDDDGIALY 142

Qy        348 VRGDAARAEVVNTVLRTAKSLAAGVSAQHGGRVTLRQTRIETAGAGAEGISVLGFE---- 403
              | |: |:| : :: |:     | ||  : |  ||::: |   |     :  |  |
Db        143 VAGEQAQASIADSTLQG----AGGVQIERGANVTVQRSAIVDGGLHIGALQSLQPEDLPP 198

Qy        404 -------------PQSGSGPASVDMQGGSITT------TGNRAAGIALTHGS-ARLEGVA 443
                          | ||: ||:| : | |  |       || ||||:|   |:   |:
Db        199 SRVVLRDTNVTAVPASGA-PAAVSVLGASELTLDGGHITGGRAAGVAAMQGAVVHLQRAT 257

Qy        444 VR-------------------------------------AEGSGSS------------- 452
              :|                                     : ||||
Db        258 IRRGDAPAGGAVPGGAVPGGAVPGGFGPGGFGPVLDGWYGVDVSGSSVELAQSIVEAPEL 317

Qy        453 --AAQLANGTLVVSAGSLASAQSGAISVTDTPLKLMPGALASSTVSVRLTDGATAQGGNG 510
                | ::  |  |  :|   ||  | :  |    :  | |   : :|: |  || |||
Db        318 GAAIRVGRGARVTVSGGSLSAPHGNVIETGGARRFAPQA---APLSITLQAGAHAQG--K 372

Qy        511 VFLQQHSTIPVAVALESGALARGDIVA------DGNK--PLDAGISLSVASGAAWHGATQ 562
                  ' .    '' . '  '' '.'''''        '    '''    ...'' ' ' '''.
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          | :    || : |  || |:|||||       |    |||    :::|| | | |||:
Db        373 ALLYRVLPEPVKLTLTGGADAQGDIVATELPSIPGTSIGPLD----VALASQARWTGATR 428

Qy        563 VLQSATLGKGGTWVVNADSRVQDMSMRG-GRVEFQAPAPEASYKTLTLQTLDGNGVFVLN 621
           : | ::    |||:  :| |  : :   | |:|| ||    :| ||: || |:|:| :|
Db        429 AVDSLSI-DNATWVMTDNSNVGALRLASDGSVDFQQPAEAGRFKVLTVNTLAGSGLFRMN 487

Qy        622 TNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTQGQGNATFRLANVGKA 681
               | :|:| |   | ||||: |||:| |  |    | || |     ||| |||
Db        488 VFADLGLSDKLVVMQDASGQHRLWVRNSGSEPASANTLL-LVQTPLGSAATFTLANKDGK 546

Qy        682 VDLGTWRYSLAEDPKTHVWSL----------------------------------QRAGQA 708
              ||:||:|| || :     |||                                   ||:
Db        547 VDIGTYRYRLAANGNGQ-WSLVGAKAPPAPKPAPQPGPQPPQPPQPQPEAPAPQPPAGRE 605

Qy        709 LSGAANAAVNAADL---SSIALAESNALDKRLGELRLRADAGGPWARTFSERQQISNRHA 765
              || |||||||   :   |::  |||||| ||||||||  |||| | | |::|||: ||
Db        606 LSAAANAAVNTGGVGLASTLWYAESNALSKRLGELRLNPDAGGAWGRGFAQRQQLDNRAG 665

Qy        766 RAYDQTVSGLEIGLDRGWSASGGRWYAGGLLGYTYADRTYPGDGGGKVKGLHVGGYAAYV 825
              | :|| |:| |:| |   : :|||: ||| |||  || : ||||    :|||||| |:
Db        666 RRFDQKVAGFELGADHAVAVAGGRWHLGGLAGYTRGDRGFTGDGGGHTDSVHVGGYATYI 725

Qy        826 GDGGYYLDTVLRLGRYDQQYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQ 885
               | |:|||  ||  | :  : :||:||  |   ||| |   ||| ||||   : || |||
Db        726 ADSGFYLDATLRASRLENDFKVAGSDGYAVKGKYRTHGVGASLEAGRRFTHADGWFLEPQ 785

Qy        886 AEVMLWRTSGKRYRASNGLRVKVDANTATLGRLGLRFGRRIALAGGNIVQPYARLGWTQE 945
              ||: ::|  |  |||:|||||: :  :: |||||  |:|| |||  |||| :    ||
Db        786 AELAVFRAGGGAYRAANGLRVRDEGGSSVLGRLGLEVGKRIELAGGRQVQPYIKASVLQE 845

Qy        946 FKSTGDVRTNGIGHAGAGRHGRVELGAGVDAALGKGHNLYASYEYAAGDRINIPWSFHAG 1005
              |   | | |||| |    |  | ||| |: ||||:||:|||||||: | :: :|||:||||
Db        846 FDGAGTVHTNGLAHDTFLDGTDAPLGLGMAAALGRGHGLYASYEYGKGDKLAMDWTFHAG 905
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Db        846 FDGAGTVHTNGIAHRTELRGTRAELGLGMAAALGRGHSLYASYEYSKGPKLAMPWTFHAG 905

Qy       1006 YRYSF 1010
              ||||:
Db        906 YRYSW 910


RESULT 6
ADZ46876
ID   ADZ46876 standard; protein; 910 AA.
XX
AC   ADZ46876;
XX
DT   15-JUN-2007  (revised)
DT   30-JUN-2005  (first entry)
XX
DE   BASB232 polypeptide encoded by Orf15.
XX
KW   BASB232; vaccine; bacterial infection; bordetella pertussis infection;
KW   antibacterial; BOND_PC; pertactin precursor;
KW   pertactin precursor [Bordetella pertussis Tohama I]; prn;
KW   pertactin outer membrane protein;
KW   pertactin outer membrane protein [Bordetella pertussis]; Pertactin;
KW   Pertactin [Bordetella pertussis]; P.69A protein;
KW   P.69A protein [Bordetella pertussis]; GO5515; GO7155; GO9405; GO16020;
KW   GO19867.
XX
OS   Bordetella pertussis.
XX
PN   WO2005032584-A2.
XX
PD   14-APR-2005.
XX
PF   01-OCT-2004; 2004WO-EP011082
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PF 01-OCT-2004; 2004WO-EP011082.
XX
PR 02-OCT-2003; 2003GB-00023112.
PR 02-OCT-2003; 2003GB-00023113.
XX
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
XX
PI Castado C, Denoel P, Godfroid F, Poolman J;
XX
DR WPI; 2005-296056/30.
DR N-PSDB; ADZ46875.
DR PC:NCBI; gi464364.
DR PC:SWISSPROT; P14283.
DR PC:BIND; 330939,330940.
XX
PT Immunogenic composition, comprises polypeptide of Bordetella pertussis or
PT mixture of different B.pertussis, antigens, useful in Bordetella disease
PT treatments.
XX
PS Claim 3; SEQ ID NO 30; 172pp; English.
XX
CC The invention relates to BASB232 polypeptides (SEQ Group 2), and the
CC polynucleotide sequences (SEQ Group 1) encoding them. The invention also
CC relates to an immunogenic composition, comprising a B. pertussis BASB232
CC polypeptide or a mixture of 2-9 or 10 different B. pertussis antigens,
CC chosen from Bordetella autotransporter protein, Bordetella iron
CC acquisition protein, Bordetella lipoprotein, Bordetella adhesin and
CC Bordetella toxin/invasin, and an excipient. Also described is a vaccine
CC comprising the above immunogenic composition. The immunogenic composition
CC is useful in the preparation of a medicament for use in the treatment or
CC prevention of Bordetella disease such as whooping cough. The immunogenic
CC composition and vaccine are useful for treating or preventing Bordetella
CC infections such as B. pertussis, B. parapertussis or B. bronchiseptica
CC infections, by administering the vaccine to a host. This sequence

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CC   infections, by administering the vaccine to a host. This sequence
CC   represents a BASB232 polypeptide of the invention.
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 910 AA;

  Query Match             25.2%;  Score 1307;  DB 10;  Length 910;
  Best Local Similarity   36.7%;  Pred. No. 4.8e-69;
  Matches  332;  Conservative  112;  Mismatches  299;  Indels  162;  Gaps   22;

Qy        247 GAPLAAHPPLDRVAAVHAGQ------------DGKVTLREVALRAHGPQATGVYAYMPGS 294
              ||  |||   :  : |  |:             |  |     ::  | || |:    | :
Db         27 GAAPAAHADWNNQSIVKTGERQHGIHIQGSDPGGVRTASGTTIKVSGRQAQGILLENPAA 86

Qy        295 EITLQGGTVSVQG---DDGAGVVAGAGLLDALPPGGTVRLDGTTVSTDGANTD----AVL 347
              |:  : |:|:  |   |||     |   : |    | :  |  |::  |    |    |:
Db         87 ELQFRNGSVTSSGQLSDDGIRRFLGTVTVKA----GKLVADHATLANVGDTWDDDGIALY 142

Qy        348 VRGDAARAEVVNTVLRTAKSLAAGVSAQHGGRVTLRQTRIETAGAGAEGISVLGFE---- 403
              | |: |:| : :: |:     | ||  : |  ||:::: |   |     :  |  |
Db        143 VAGEQAQASIADSTLQG----AGGVQIERGANVTVQRSAIVDGGLHIGALQSLQPEDLPP 198

Qy        404 -------------PQSGSGPASVDMQGGSITT------TGNRAAGIALTHGS-ARLEGVA 443
                          | ||: ||:| : | |  |       || ||||:|   |:   |:
Db        199 SRVVLRDTNVTAVPASGA-PAAVSVLGASELTLDGGHITGGRAAGVAAMQGAVVHLQRAT 257

Qy        444 VR-------------------------------------AEGSGSS------------- 452
              :|                                     : ||||
Db        258 IRRGDAPAGGAVPGGAVPGGAVPGGFGPGGFGPVLDGWYGVDVSGSSVELAQSIVEAPEL 317

Qy        453 --AAQLANGTLVVSAGSLASAQSGAISVTDTPLKLMPGALASSTVSVRLTDGATAQGGNG 510
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                 | ::  |  |  :|   ||  | :  |    :  | |   : :|: |  || |||
Db        318 GAAIRVGRGARVTVSGGSLSAPHGNVIETGGARRFAPQA---APLSITLQAGAHAQG--K 372

Qy        511 VFLQQHSTIPVAVALESGALARGDIVA------DGNK--PLDAGISLSVASGAAWHGATQ 562
                | :    || : |  || |:|||||       |    |||    :::|| | | |||:
Db        373 ALLYRVLPEPVKLTLTGGADAQGDIVATELPSIPGTSIGPLD----VALASQARWTGATR 428

Qy        563 VLQSATLGKGGTWVVNADSRVQDMSMRG-GRVEFQAPAPEASYKTLTLQTLDGNGVFVLN 621
                : | ::    |||:  :| |  : :   | |:|| ||    :| ||: || |:|:| :|
Db        429 AVDSLSI-DNATWVMTDNSNVGALRLASDGSVDFQQPAEAGRFKVLTVNTLAGSGLFRMN 487

Qy        622 TNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTQGQGNATFRLANVGKA 681
                    | :|:| |   | ||||: |||:| |  |    | || |     ||| |||
Db        488 VFADLGLSDKLVVMQDASGQHRLWVRNSGSEPASANTLL-LVQTPLGSAATFTLANKDGK 546

Qy        682 VDLGTWRYSLAEDPKTHVWSL---------------------------------QRAGQA 708
                ||:||:|| || :     |||                                   ||:
Db        547 VDIGTYRYRLAANGNGQ-WSLVGAKAPPAPKPAPQPGPQPPQPPQPQPEAPAPQPPAGRE 605

Qy        709 LSGAANAAVNAADL---SSIALAESNALDKRLGELRLRADAGGPWARTFSERQQISNRHA 765
                || |||||||   :   |::  |||||| |||||||  |||| | | |::|||: ||
Db        606 LSAAANAAVNTGGVGLASTLWYAESNALSKRLGELRLNPDAGGAWGRGFAQRQQLDNRAG 665

Qy        766 RAYDQTVSGLEIGLDRGWSASGGRWYAGGLLGYTYADRTYPGDGGGKVKGLHVGGYAAYV 825
                | :|| |:| |:| |   : :|||: ||| |||  || : |||||    :|||||| |:
Db        666 RRFDQKVAGFELGADHAVAVAGGRWHLGGLAGYTRGDRGFTGDGGGHTDSVHVGGYATYI 725

Qy        826 GDGGYYLDTVLRLGRYDQQYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQ 885
                 | |:|||  ||  | :  : :||:||  |   ||| |   ||| ||||   : || |||
Db        726 ADSGFYLDATLRASRLENDFKVAGSDGYAVKGKYRTHGVGASLEAGRRFTHADGWFLEPQ 785

Qy        886 AEVMLWRTSGKRYRASNGLRVKVDANTATLGRLGLRFGRRIALAGGNIVQPYARLGWTQE 945
                ||: ::|  |  |||:|||||: :  :: ||||||  |:|| ||||  |||| :    ||
Db        786 AELAVTPAGGGAYRAANGLRVPDPGGGSVLGRLGLEVGKRIPLAGGPQVQPYIKASWLQE 845
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```
Db        786 AELAVFRAGGGAYRAANGLRVRDEGGSSVLGRLGLEVGKRIELAGGRQVQPYIKASVLQE 845

Qy        946 FKSTGDVRTNGIGHAGAGRHGRVELGAGVDAALGKGHNLYASYEYAAGDRINIPWSFHAG 1005
              |   | | |||| |    |  | ||| |: ||||:||:|||||||: | :: :|||||||
Db        846 FDGAGTVHTNGIAHRTELRGTRAELGLGMAAALGRGHSLYASYEYSKGPKLAMPWTFHAG 905

Qy       1006 YRYSF 1010
              ||||:
Db        906 YRYSW 910


RESULT 7
ADZ39252
ID   ADZ39252 standard; protein; 915 AA.
XX
AC   ADZ39252;
XX
DT   15-JUN-2007  (revised)
DT   30-JUN-2005  (first entry)
XX
DE   Pertussis toxin P69 pertactin protein.
XX
KW   Prion protein; fusion protein; protein engineering; vaccine;
KW   prion infection; cerebroprotective; infection; prion disease;
KW   degeneration; neurological disease;
KW   transmissible spongiform encephalopathy; Creutzfeldt Jakob disease;
KW   neuroprotective; BSE; scrapie; kuru; P69; toxin; BOND_PC;
KW   pertactin outer membrane protein;
KW   pertactin outer membrane protein [Bordetella pertussis]; pertactin;
KW   pertactin [Bordetella pertussis]; P.69B protein;
KW   P.69B protein [Bordetella pertussis]; GO7155; GO5524; GO9405.
XX
OS   Bordetella pertussis.
XX
```

XX

PN WO2005034995-A1.

XX

PD 21-APR-2005.

XX

PF 30-SEP-2003; 2003WO-US031057.

XX

PR 10-SEP-2003; 2003US-0502032P.

XX

PA (CHIR) CHIRON CORP.

XX

PI Abrignani S, Cohen F, Michelitsch MD, Hu CY, Phelps B;

XX

DR WPI; 2005-306277/31.

DR PC:NCBI; gi15213624.

XX

PT Generating antibodies specific to pathogenic prion, useful in detecting
PT presence of pathogenic prion, involves administering prion chimera having
PT prion protein and non-prion, beta-helical protein, to animal.

XX

PS Claim 9; SEQ ID NO 3; 173pp; English.

XX

CC The invention relates to generating (M1) antibodies specific to a
CC pathogenic prion, comprising administering to an animal a prion chimera
CC (PC), where PC comprises a prion protein (PrP) or its fragment or
CC derivative, and a non-prion, beta-helical protein or its fragment or
CC derivative. Also included are an antibody (I) specific to PC, a
CC polynucleotide (P1) encoding (I), detecting the presence of pathogenic
CC prion in a biological sample, a solid support comprising (I) bound to it,
CC a solid support for use in immunoassay (comprising at least one antibody
CC specific to pathogenic and nonpathogenic prions bound to it), a kit for
CC detecting the presence of a pathogenic prion in a biological sample, an
CC immunogenic composition (C1) (comprising a PC and an adjuvant, or a
CC polynucleotide encoding PC and an adjuvant) and treating or preventing

CC polynucleotide encoding PC and an adjuvant) and treating or preventing
CC (M2) a pathogenic prion related disease, involves administering PC to an
CC animal. The PrP or its fragment or derivative has a beta-helical
CC conformation of a pathogenic prion, and comprises fa fragment
CC corresponding to amino acids 126-154 or 135-155 of the full length human
CC or mouse prion (PrP) protein. The non-prion-beta-helical protein is a
CC left handed helical protein or right handed helical protein. The non-
CC prion-beta-helical protein is derived from Pertussis toxin P69 pertactin
CC (fragments used are designated Control A or Control B) or gamma carbonic
CC anhydrase (GCA, fragments used also designated Control A and Control B
CC (optionally lacking the leader peptide)). The PC further comprises a tag
CC sequence, where the tag sequence is a histidine tag sequence, and may
CC include a tpa leader peptide (not defined). The method is useful for
CC generating antibodies specific to pathogenic prion. The antibody is
CC useful for raising an immune response to a pathogenic prion, which
CC involves administering the antibody to an animal. The antibody is useful
CC for detecting the presence of pathogenic prion in a biological sample.
CC The immunogenic composition is useful for raising an immune response to a
CC pathogenic prion. The methods, antibodies and compositions are useful for
CC treating or preventing a pathogenic prion related disease including
CC transmissible spongiform encephalopathies, Creutzfeldt-Jacob disease,
CC Gerstmann-Straussler-Scheinker syndrome, Fatal familial insomnia, bovine
CC spongiform encephalopathies, transmissible mink encephalopathies,
CC scrapie, mad cow disease, feline spongiform encephalopathies and kuru.
CC The present sequence is the full length P69 protein.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 915 AA;

Query Match 25.2%; Score 1304.5; DB 10; Length 915;
Best Local Similarity 36.5%; Pred. No. 6.8e-69;
Matches 332; Conservative 112; Mismatches 209; Indels 167; Gaps 22;

```
  Matches  332;  Conservative  112;  Mismatches  299;  Indels  167;  Gaps   22;

Qy        247 GAPLAAHPPLDRVAAVHAGQ------------DGKVTLREVALRAHGPQATGVYAYMPGS 294
              ||  |||   :  : |  |:             |  |     ::  | || |:    | :
Db         27 GAAPAAHADWNNQSIVKTGERQHGIHIQGSDPGGVRTASGTTIKVSGRQAQGILLENPAA 86

Qy        295 EITLQGGTVSVQG---DDGAGVVAGAGLLDALPPGGTVRLDGTTVSTDGANTD----AVL 347
              |:  : |:|:  |   |||     |   : |    | :  |  |::  |   |    |:
Db         87 ELQFRNGSVTSSGQLSDDGIRRFLGTVTVKA----GKLVADHATLANVGDTWDDDGIALY 142

Qy        348 VRGDAARAEVVNTVLRTAKSLAAGVSAQHGGRVTLRQTRIETAGAGAEGISVLGFE---- 403
              | |: |:| : :: |:     | ||  : |  ||:::: |   |     :  |  |
Db        143 VAGEQAQASIADSTLQG----AGGVQIERGANVTVQRSAIVDGGLHIGALQSLQPEDLPP 198

Qy        404 -------------PQSGSGPASVDMQGGSITT------TGNRAAGIALTHGS-ARLEGVA 443
                          | ||: ||:| : | |  |       || ||||:|   |:   |:
Db        199 SRVVLRDTNVTAVPASGA-PAAVSVLGASELTLDGGHITGGRAAGVAAMQGAVVHLQRAT 257

Qy        444 VR---------------------------------------------AEGSGSS-------- 452
              :|                                             : ||||
Db        258 IRRGDAPAGGAVPGGAVPGGFGPGGFGPGGFGPGGFGPVLDGWYGVDVSGSSVELAQSIV 317

Qy        453 -------AAQLANGTLVVSAGSLASAQSGAISVTDTPLKLMPGALASSTVSVRLTDGATA 505
                    | ::  |  |  :|   ||  | :  |    :  | |   : :|: |  || |
Db        318 EAPELGAAIRVGRGARVTVSGGSLSAPHGNVIETGGARRFAPQA---APLSITLQAGAHA 374

Qy        506 QGGNGVFLQQHSTIPVAVALESGALARGDIVA------DGNK--PLDAGISLSVASGAAW 557
              ||      | :    || : |  || |:|||||       |    |||    :::|| | |
Db        375 QG--KALLYRVLPEPVKLTLTGGADAQGDIVATELPSIPGTSIGPLD----VALASQARW 428

Qy        558 HGATQVLQSATLGKGGTWVVNADSRVQDMSMRG-GRVEFQAPAPEASYKTLTLQTLDGNG 616
               |||: : | ::    |||:  :| |  : :   | |:|| ||    :| ||: || |:|
Db        429 TGATRAVDSLSI-DNATWVMTDNSNVGALRLASDGSVDFQQPAEAGRFKVLTVNTLAGSG 487
```

```
Qy        617 VFVLNTNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTQGQGNATFRLA 676
              :| :|     | :|:| |   | ||||: |||:| |  |    | || |     ||| ||
Db        488 LFRMNVFADLGLSDKLVVMQDASGQHRLWVRNSGSEPASANTLL-LVQTPLGSAATFTLA 546

Qy        677 NVGKAVDLGTWRYSLAEDPKTHVWSL---------------------------------Q 703
              |    ||:||:|| || :     |||
Db        547 NKDGKVDIGTYRYRLAANGNGQ-WSLVGAKAPPAPKPAPQPGPQPPQPPQPQPEAPAPQP 605

Qy        704 RAGQALSGAANAAVNAADL---SSIALAESNALDKRLGELRLRADAGGPWARTFSERQQI 760
               ||: || |||||||   :   |::  |||||| ||||||||  |||| | | |::|||:
Db        606 PAGRELSAAANAAVNTGGVGLASTLWYAESNALSKRLGELRLNPDAGGAWGRGFAQRQQL 665

Qy        761 SNRHARAYDQTVSGLEIGLDRGWSASGGRWYAGGLLGYTYADRTYPGDGGGKVKGLHVGG 820
               ||  | :|| |:| |:| |   : :|||||: ||| |||  || : |||||    :||||
Db        666 DNRAGRRFDQKVAGFELGADHAVAVAGGRWHLGGLAGYTRGDRGFTGDGGGHTDSVHVGG 725

Qy        821 YAAYVGDGGYYLDTVLRLGRYDQQYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELPNDW 880
              || |: | |:|||  ||  | :  : :||:||  |   ||| |   ||| ||||   : |
Db        726 YATYIADSGFYLDATLRASRLENDFKVAGSDGYAVKGKYRTHGVGASLEAGRRFTHADGW 785

Qy        881 FAEPQAEVMLWRTSGKRYRASNGLRVKVDANTATLGRLGLRFGRRIALAGGNIVQPYARL 940
              | |||||: ::|  |  |||:|||||: :  :: |||||  |:|| ||||  |||| :
Db        786 FLEPQAELAVFRAGGGAYRAANGLRVRDEGGSSVLGRLGLEVGKRIELAGGRQVQPYIKA 845

Qy        941 GWTQEFKSTGDVRTNGIGHAGAGRHGRVELGAGVDAALGKGHNLYASYEYAAGDRINIPW 1000
                 |||   | | |||| |    |  | ||| |: ||||:||:|||||||: | :: :||
Db        846 SVLQEFDGAGTVHTNGIAHRTELRGTRAELGLGMAAALGRGHSLYASYEYSKGPKLAMPW 905

Qy       1001 SFHAGYRYSF 1010
              :||||||||:
Db        906 TFHAGYRYSW 915
```

```
RESULT 8
AAR14320
ID   AAR14320 standard; protein; 911 AA.
XX
AC   AAR14320;
XX
DT   25-MAR-2003  (revised)
DT   20-JAN-1992  (first entry)
XX
DE   Pertactin antigen P.68.
XX
KW   Pertactin; Pichia; B. pertussis; B. parapertussis.
XX
OS   Bordetella bronchiseptica.
XX
FH   Key             Location/Qualifiers
FT   Peptide         266. .270
FT                   /label= repeat
FT   Peptide         271. .275
FT                   /label= repeat
FT   Peptide         570. .572
FT                   /label= repeat
FT   Peptide         574. .576
FT                   /label= repeat
FT   Peptide         578. .580
FT                   /label= repeat
FT   Peptide         581. .583
FT                   /label= repeat
FT   Peptide         584. .586
FT                   /label= repeat
FT   Peptide         587. .589
FT                   /label= repeat
FT   Peptide         590. .601
```

FT Peptide 599. .601
FT /label= repeat
XX
PN WO9115571-A.
XX
PD 17-OCT-1991.
XX
PF 02-APR-1990; 90GB-00007416.
XX
PR 02-APR-1990; 90GB-00007416.
XX
PA (WELL) WELLCOME FOUND LTD.
XX
PI Clare JJ, Romanos MA;
XX
DR WPI; 1991-325214/44.
DR N-PSDB; AAQ14319.
XX
PT Pichia microorganism transformants - for production of Bordetella
PT pertactin antigens for whooping cough vaccines.
XX
PS Disclosure; Fig 1B; 38pp; English.
XX
CC Pichia microorganisms are transformed for the expression of pertactin
CC antigens. DNA sequence used are represented in AAQ14319-20 encoding the
CC B. bronchiseptica P.68 and B. parapertussis P.70 antigen respectively or
CC the B. pertussis P.69 encoding sequence described by I.G. Charles et al.
CC Proc. Natl. Acad. Sci. USA, Vol. 80:3554-3448 (1989). (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
SQ Sequence 911 AA;

Query Match 25.1%; Score 1299.5; DB 2; Length 911;
Best Local Similarity 36.6%; Pred. No. 1.3e-68;

```
 Best Local Similarity   36.6%;  Pred. No. 1.3e-68;
 Matches  330;  Conservative  117;  Mismatches  300;  Indels  155;  Gaps   23;

Qy        247 GAPLAAHPPLDRVAAVHAGQ----------DGKVTLREVALRAHGPQATGVYAYMPGS 294
              ||  |||   :  : : ||:             |  |     ::  | || ||    | :
Db         27 GAAPAAHADWNNQSIIKAGERQHGIHIKQSDGAGVRTATGTTIKVSGRQAQGVLLENPAA 86

Qy        295 EITLQGGTVSVQG---DDGAGVVAGAGLLDALPPGGTVRLDGTTVS--TDGANTD--AVL 347
              |:  | |:|:  |   |:|     |   : |    | :  |  |::  :|  : |  |:
Db         87 ELRFQNGSVTSSGQLFDEGVRRFLGTVTVKA----GKLVADHATLANVSDTRDDDGIALY 142

Qy        348 VRGDAARAEVVNTVLRTAKSLAAGVSAQHGGRVTLRQTRIETAGAGAEGISVLGFE---- 403
              | |: |:| : :: |:     | ||  : |  ||:::: |   |     :  |  |
Db        143 VAGEQAQASIADSTLQG----AGGVRVERGANVTVQRSTIVDGGLHIGTLQPLQPEDLPP 198

Qy        404 -------------PQSGSGPASVDMQGGSITT------TGNRAAGIALTHGS-ARLEGVA 443
                          | ||: ||:| : | :  |       || ||||:|   |:   |:
Db        199 SRVVLGDTSVTAVPASGA-PAAVSVFGANELTVDGGHITGGRAAGVAAMDGAIVHLQRAT 257

Qy        444 VR---AEGSGS---------------------------------SAAQLA-------NG 459
              :|   |   |:                                  | ||
Db        258 IRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQSIVEAPQLGAAIRAGRGA 317

Qy        460 TLVVSAGSLASAQSGAISVTDTPLKLMPGALASSTVSVRLTDGATAQGGNGVFLQQHSTI 519
               : || |||::     |       :  | |   | :|: |  || |||     | :
Db        318 RVTVSGGSLSAPHGNVIETGGGARRFPPPA---SPLSITLQAGARAQG--RALLYRVLPE 372

Qy        520 PVAVALESGALARGDIVADGNKPLDAG----ISLSVASGAAWHGATQVLQSATLGKGGTW 575
              || : |  ||  :|||||    |:       : :::|| | | |||: : | ::    ||
Db        373 PVKLTLAGGAQGQGDIVATELPPIPGASSGPLDVALASQARWTGATRAVDSLSI-DNATW 431

Qy        576 VVNADSRVQDMSMRG-GRVEFQAPAPEASYKTLTLQTLDGNGVFVLNTNVAAGQNDQLRV 634
              |:  :| |  : :   | |:|| ||     :| | : || |:|:| :|     | :|:| |
Db        432 VMTPNGNVGALPLASDGGVDPQQPAFAGPPKGLMVDTLAGSGLFDMNTTADLGLSPKLVV 491
```

```
Db        432 VMTDNSNVGALRLASDGSVDFQQPAEAGRFKCLMVDTLAGSGLFRMNVFADLGLSDKLVV 491

Qy        635 TGRADGQHRVLVRNAGGEADSRGARLGLVHTQGQGNATFRLANVGKAVDLGTWRYSLAED 694
                 | ||||:||||:| |  | |  : || |     ||| |||    ||:||:|| || :
Db        492 MRDASGQHRLLVRNSGSEPAS-GNTMLLVQTPRGSAATFTLANKDGKVDIGTYRYRLAAN 550

Qy        695 PKTHVWSL---------------------------------QR----------AGQALSG 711
                  |||                                   ||          ||: ||
Db        551 GNGQ-WSLVGAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSA 609

Qy        712 AANAAVNAADL---SSIALAESNALDKRLGELRLRADAGGPWARTFSERQQISNRHARAY 768
                  |||||||   :   |::  |||||| |||||||  |||| | | |::|||: ||  | :
Db        610 AANAAVNTGGVGLASTLWYAESNALSKRLGELRLNPDAGGAWGRGFAQRQQLDNRAGRRF 669

Qy        769 DQTVSGLEIGLDRGWSASGGRWYAGGLLGYTYADRTYPGDGGGKVKGLHVGGYAAYVGDG 828
                  || |:| |:| |   : :|||: ||| |||  || : |||||    :|||||| |: :
Db        670 DQKVAGFELGADHAVAVAGGRWHLGGLAGYTRGDRGFTGDGGGHTDSVHVGGYATYIANS 729

Qy        829 GYYLDTVLRLGRYDQQYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQAEV 888
                  |:|||  ||  | :  : :||:||  |   ||| |   ||| ||||   : || |||||:
Db        730 GFYLDATLRASRLENDFKVAGSDGYAVKGKYRTHGVGASLEAGRRFAHADGWFLEPQAEL 789

Qy        889 MLWRTSGKRYRASNGLRVKVDANTATLGRLGLRFGRRIALAGGNIVQPYARLGWTQEFKS 948
                   ::|  |  |||:|||||: :  :: ||||||  |:|| ||||  |||| :    |||
Db        790 AVFRVGGGSYRAANGLRVRDEGGSSVLGRLGLEVGKRIELAGGRQVQPYIKASVLQEFDG 849

Qy        949 TGDVRTNGIGHAGAGRHGRVELGAGVDAALGKGHNLYASYEYAAGDRINIPWSFHAGYRY 1008
                   | |||||| |     |  | ||| |: ||||:||:|||||||: | :: :||:|||||||
Db        850 AGTVRTNGIAHRTELRGTRAELGLGMAAALGRGHSLYASYEYSKGPKLAMPWTFHAGYRY 909

Qy       1009 SF 1010
                 |:
Db        910 SW 911
```

```
RESULT 9
AAE16183
ID   AAE16183 standard; protein; 911 AA.
XX
AC   AAE16183;
XX
DT   15-JUN-2007  (revised)
DT   26-MAR-2002  (first entry)
XX
DE   Bordetella bronchiseptica pertactin outer membrane protein, p.68.
XX
KW   Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
KW   therapy; antibiotic; antibacterial; p.68; BOND_PC; P.68 Peractin;
KW   P.68 Peractin [Bordetella bronchiseptica]; GO5515; GO5524; GO7155;
KW   GO9405; GO16020; GO19867.
XX
OS   Bordetella bronchiseptica.
XX
FH   Key             Location/Qualifiers
FT   Region          254. .299
FT                   /note= "Pertactin region I"
FT   Region          559. .610
FT                   /note= "Pertactin region II"
XX
PN   WO200190143-A2.
XX
PD   29-NOV-2001.
XX
PF   23-MAY-2001; 2001WO-EP006457.
XX
PR   25-MAY-2000; 2000US-0206969P.
XX
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XX

PA (INSP) INST PASTEUR.

XX

PI Guiso-Maclouf N, Boursaux-Eude C;

XX

DR WPI; 2002-097639/13.

DR N-PSDB; AAD26440.

DR PC:NCBI; gi39397.

DR PC:SWISSPROT; Q03035.

XX

PT Polypeptides containing polymorphisms of the repeated regions of

PT pertactin in Bordetella species, useful in immunogenic compositions for

PT treating infections caused by Bordetella and in diagnostic methods.

XX

PS Disclosure; Page 28; 47pp; English.

XX

CC The present invention relates to Bordetella bronchiseptica pertactin

CC (outer membrane protein) or their fragments. Pertactin (PRN) is used as

CC vaccine. Pertactin antibody is useful for treating Bordetella infections

CC and used to detect Bordetella antigens in biological preparations or in

CC purifying corresponding proteins, glycoproteins or their mixtures when

CC used in affinity chromatographic columns. Pertactin is useful as antigens

CC to identify antibodies to Bordetella in materials such as human or other

CC animal tissue and human or other animal cells, as well as biological

CC fluids, such as human or other animal body fluids, including human sera,

CC and to determine the concentration of Ab in those materials. Thus the

CC antigens can be used for qualitative or quantitative determination of

CC Bordetella in a material. The present sequence is B. bronchiseptica

CC pertactin outer membrane protein, p.68

CC

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed

CC information from BOND.

XX

SQ Sequence 911 AA;

```
SQ   Sequence 911 AA;

  Query Match             25.0%;  Score 1293.5;  DB 5;  Length 911;
  Best Local Similarity   36.5%;  Pred. No. 3e-68;
  Matches  329;  Conservative  118;  Mismatches  300;  Indels  155;  Gaps   23;

Qy        247 GAPLAAHPPLDRVAAVHAGQ------------DGKVTLREVALRAHGPQATGVYAYMPGS 294
              ||  ||:   :  : : ||:              |  |     ::  | || ||    | :
Db         27 GAAPAAYADWNNQSIIKAGERQHGIHIKQSDGAGVRTATGTTIKVSGRQAQGVLLENPAA 86

Qy        295 EITLQGGTVSVQG---DDGAGVVAGAGLLDALPPGGTVRLDGTTVS--TDGANTD--AVL 347
              |:  | |:|:  |   |:|     |   : |    | :  |  |::  :|  : |  |:
Db         87 ELRFQNGSVTSSGQLFDEGVRRFLGTVTVKA----GKLVADHATLANVSDTRDDDGIALY 142

Qy        348 VRGDAARAEVVNTVLRTAKSLAAGVSAQHGGRVTLRQTRIETAGAGAEGISVLGFE---- 403
              | |: |:| : :: |:     | ||  : |  ||:::: |   |     :  |  |
Db        143 VAGEQAQASIADSTLQG----AGGVRVERGANVTVQRSTIVDGGLHIGTLQPLQPEDLPP 198

Qy        404 -------------PQSGSGPASVDMQGGSITT------TGNRAAGIALTHGS-ARLEGVA 443
                          | ||: ||:| : | :  |      || ||||:|   |:   |:
Db        199 SRVVLGDTSVTAVPASGA-PAAVSVFGANELTVDGGHITGGRAAGVAAMDGAIVHLQRAT 257

Qy        444 VR---AEGSGS---------------------------------SAAQLA-------NG 459
              :|   |   |:                                 | ||
Db        258 IRRGDAPAGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQSIVEAPQLGAAIRAGRGA 317

Qy        460 TLVVSAGSLASAQSGAISVTDTPLKLMPGALASSTVSVRLTDGATAQGGNGVFLQQHSTI 519
               : || |||::     |       :  | |   | :|: |  || |||     | :
Db        318 RVTVSGGSLSAPHGNVIETGGGARRFPPPA---SPLSITLQAGARAQG--RALLYRVLPE 372

Qy        520 PVAVALESGALARGDIVADGNKPLDAG----ISLSVASGAAWHGATQVLQSATLGKGGTW 575
              || : |  ||  :|||||    |:       : :::|| | | |||: : | ::    ||
Db        373 PVKLTLAGGAQGQGDIVATELPPIPGASSGPLDVALASQARWTGATRAVDSLSI-DNATW 431
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```
Qy        576 VVNADSRVQDMSMRG-GRVEFQAPAPEASYKTLTLQTLDGNGVFVLNTNVAAGQNDQLRV 634
              |:  :| |  : :    | |:|| ||    :| | : || |:|:| :|     | :|:| |
Db        432 VMTDNSNVGALRLASDGSVDFQQPAEAGRFKCLMVDTLAGSGLFRMNVFADLGLSDKLVV 491

Qy        635 TGRADGQHRVLVRNAGGEADSRGARLGLVHTQGQGNATFRLANVGKAVDLGTWRYSLAED 694
                 | ||||:||||:| |  | |  : || |     ||| |||    ||:||:|| || :
Db        492 MRDASGQHRLLVRNSGSEPAS-GNTMLLVQTPRGSAATFTLANKDGKVDIGTYRYRLAAN 550

Qy        695 PKTHVWSL---------------------------------QR----------AGQALSG 711
                   |||                                 ||          ||: ||
Db        551 GNGQ-WSLVGAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQRQPEAPAPQPPAGRELSA 609

Qy        712 AANAAVNAADL---SSIALAESNALDKRLGELRLRADAGGPWARTFSERQQISNRHARAY 768
              |||||||   :   |::  |||||| |||||||  |||| | | |::|||: ||  | :
Db        610 AANAAVNTGGVGLASTLWYAESNALSKRLGELRLNPDAGGAWGRGFAQRQQLDNRAGRRF 669

Qy        769 DQTVSGLEIGLDRGWSASGGRWYAGGLLGYTYADRTYPGDGGGKVKGLHVGGYAAYVGDG 828
              || |:| |:| |   : :|||: ||| |||  || : |||||    :|||||| |: :
Db        670 DQKVAGFELGADHAVAVAGGRWHLGGLAGYTRGDRGFTGDGGGHTDSVHVGGYATYIANS 729

Qy        829 GYYLDTVLRLGRYDQQYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQAEV 888
              |:|||  ||  | :  : :||:||  |   ||| |   ||| ||||   : || |||||:
Db        730 GFYLDATLRASRLENDFKVAGSDGYAVKGKYRTHGVGASLEAGRRFAHADGWFLEPQAEL 789

Qy        889 MLWRTSGKRYRASNGLRVKVDANTATLGRLGLRFGRRIALAGGNIVQPYARLGWTQEFKS 948
              ::|  |  |||:|||||: :  :: ||||||  |:|| |||  |||| :    |||
Db        790 AVFRVGGGSYRAANGLRVRDEGGSSVLGRLGLEVGKRIELAGGRQVQPYIKASVLQEFDG 849

Qy        949 TGDVRTNGIGHAGAGRHGRVELGAGVDAALGKGHNLYASYEYAAGDRINIPWSFHAGYRY 1008
               | |||||| |     |  | ||| |: ||||:||:|||||||: | :: :||:|||||||
Db        850 AGTVRTNGIAHRTELRGTRAELGLGMAAALGRGHSLYASYEYSKGPKLAMPWTFHAGYRY 909

Qy       1009 SE 1010
```

```
Qy       1009 SF 1010
              |:
Db        910 SW 911


RESULT 10
AAR25578
ID   AAR25578 standard; protein; 922 AA.
XX
AC   AAR25578;
XX
DT   15-JUN-2007  (revised)
DT   25-MAR-2003  (revised)
DT   08-JAN-1993  (first entry)
XX
DE   Bordetella parapertussis P95 antigen precursor.
XX
KW   Whooping cough; P70 antigen; P95 precursor protein; vaccination; BOND_PC;
KW   pertactin precursor;
KW   pertactin precursor [Bordetella parapertussis 12822]; prn; pertactin;
KW   pertactin [Bordetella parapertussis];
KW   pertactin precursor [Bordetella parapertussis]; GO5515; GO7155; GO9405;
KW   GO16020; GO19867.
XX
OS   Bordetella parapertussis.
XX
FH   Key             Location/Qualifiers
FT   Protein         35. .643
FT                   /label= P70
FT   Binding-site    260. .262
FT                   /note= "motif associated with cell-cell adhesion"
FT   Region          266. .285
FT                   /note= "contains 5 direct, tandem repeats"
FT   Region          575. .612
```

```
FT   Region          575. .612
FT                   /note= "contains 9 direct repeats of Pro-Gln-Pro"
FT   Binding-site    712. .714
FT                   /note= "motif associated with cell-cell adhesion"
XX
PN   WO9211292-A1.
XX
PD   09-JUL-1992.
XX
PF   23-DEC-1991;   91WO-GB002302.
XX
PR   21-DEC-1990;   90GB-00027901.
XX
PA   (WELL ) WELLCOME FOUND LTD.
XX
PI   Charles IG;
XX
DR   WPI; 1992-250033/30.
DR   N-PSDB; AAQ26509.
DR   PC:NCBI; gi129828.
DR   PC:SWISSPROT; P24328.
XX
PT   Acellular vaccine for immunisation against whooping cough - comprises
PT   protein uncontaminated by B. para:pertussis components and capable of
PT   binding antibodies which bind native P70 antigen.
XX
PS   Claim 1; Fig 1; 20pp; English.
XX
CC   A cosmid library was constructed by transforming E.coli HB101 with
CC   recombinant cosmids prepared by partial digestion of B.parapertussis
CC   chromosomal DNA with Sau3A and cloning of 40-50kb fragments into the
CC   BamHI site of cosmid pHC79. The cosmids were screened with a 1.8kb ClaI
CC   fragment from the prn gene of B.pertussis. The insert from one positive
CC   colony harbouring cosmid pPD911 was sequenced and found to contain an
```

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CC   colony, harbouring cosmid pBD811, was sequenced and found to contain an
CC   open reading frame encoding a 922 amino acid protein with calculated
CC   mol.wt. 95,177. This precursor protein ("P95") is processed in vivo to
CC   the P70 antigen of apparent mol. wt. 70,000 as determined by SDS-PAGE,
CC   but with actual mol.wt. 61kD. Antigenic fragments of the protein will be
CC   useful in developing an acellular vaccine against B.parapertussis.
CC   Preferred fragments include amino acids Pro577 to Pro612 or Ala574 to
CC   Pro612. (Updated on 25-MAR-2003 to correct PN field.)
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 922 AA;

  Query Match             24.7%;  Score 1280;  DB 2;  Length 922;
  Best Local Similarity   35.9%;  Pred. No. 2e-67;
  Matches  328;  Conservative  118;  Mismatches  301;  Indels  166;  Gaps   23;

Qy        247 GAPLAAHPPLDRVAAVHAGQ------------DGKVTLREVALRAHGPQATGVYAYMPGS 294
              ||  ||:   :  : : ||:              |  |     ::  | || ||    | :
Db         27 GAAPAAYADWNNQSIIKAGERQHGIHIKQSDGAGVRTATGTTIKVSGRQAQGVLLENPAA 86

Qy        295 EITLQGGTVSVQG---DDGAGVVAGAGLLDALPPGGTVRLDGTTVS--TDGANTD--AVL 347
              |:  | |:|:  |   |:|      |   : |    | :  |  |::  :|  : |  |:
Db         87 ELRFQNGSVTSSGQLFDEGVRRFLGTVTVKA----GKLVADHATLANVSDTRDDDGIALY 142

Qy        348 VRGDAARAEVVNTVLRTAKSLAAGVSAQHGGRVTLRQTRIETAGAGAEGISVLGFE---- 403
              | |: |:| : :: |:     | ||  : |  ||:::: |   |     :  |  |
Db        143 VAGEQAQASIADSTLQG----AGGVRVERGANVTVQRSTIVDGGLHIGTLQPLQPEDLPP 198

Qy        404 -------------PQSGSGPASVDMQGGSITT------TGNRAAGIALTHGS-ARLEGVA 443
                          | ||: ||:| : | :  |       || ||||:|   |:   |:
Db        199 SRVVLGDTSVTAVPASGA-PAAVFVFGANELTVDGGHITGGRAAGVAAMDGAIVHLQRAT 257
```

```
Qy        444 VR---AEGSGS-------------------------------------SAAQLA---- 457
              :|   |   |:                                        | ||
Db        258 IRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQSIVEAPQLGAAIR 317

Qy        458 ---NGTLVVSAGSLASAQSGAISVTDTPLKLMPGALASSTVSVRLTDGATAQGGNGVFLQ 514
                    : || |||::     |       :  | |   | :|: |  || |||     |
Db        318 AGRGARVTVSGGSLSAPHGNVIETGGGARRFPPPA---SPLSITLQAGARAQG--RALLY 372

Qy        515 QHSTIPVAVALESGALARGDIVADGNKPLDAG----ISLSVASGAAWHGATQVLQSATLG 570
              :    || : |  ||  :|||||    |:       : :::|| | | |||: : | ::
Db        373 RVLPEPVKLTLAGGAQGQGDIVATELPPIPGASSGPLDVALASQARWTGATRAVDSLSI- 431

Qy        571 KGGTWVVNADSRVQDMSMRG-GRVEFQAPAPEASYKTLTLQTLDGNGVFVLNTNVAAGQN 629
                 |||:  :| |  : :   | |:|| ||    :| | : || |:|:| :|     | :
Db        432 DNATWVMTDNSNVGALRLASDGSVDFQQPAEAGRFKVLMVDTLAGSGLFRMNVFADLGLS 491

Qy        630 DQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTQGQGNATFRLANVGKAVDLGTWRY 689
              |:| |   | ||||: |||:| |  | |  : || |     ||| |||    ||:||:||
Db        492 DKLVVMRDASGQHRLWVRNSGSEPAS-GNTMLLVQTPRGSAATFTLANKDGKVDIGTYRY 550

Qy        690 SLAEDPKTHVWSL----------------------------------------QR------ 704
               || :     |||                                        ||
Db        551 RLAANGNGQ-WSLVGAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPA 609

Qy        705 ----AGQALSGAANAAVNAADL---SSIALAESNALDKRLGELRLRADAGGPWARTFSER 757
                  ||: || |||||||   :   |::  |||||| ||||||||  |||| | | |::|
Db        610 PQPPAGRELSAAANAAVNTGGVGLASTLWYAESNALSKRLGELRLNPDAGGAWGRGFAQR 669

Qy        758 QQISNRHARAYDQTVSGLEIGLDRGWSASGGRWYAGGLLGYTYADRTYPGDGGGKVKGLH 817
              ||: ||  | :|| |:| |:| |   : :||||: ||| |||  || : |||||    :|
Db        670 QQLDNRAGRRFDQKVAGFELGADHAVAVAGGRWHLGGLAGYTRGDRGFTGDGGGHTDSVH 729

Qy        818 VGGVAAVVGDGGVKLDTVLRLGRYDQQVNLAGTDGGDVTADYDTGAAWGLEGGDDEELD 877
```

```
Qy        818 VGGYAAYVGDGGYYLDTVLRLGRYDQQYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELP 877
              ||||| |: : |:|||  ||  | :  : :||:||  |   ||| |   ||| ||||
Db        730 VGGYATYIANSGFYLDATLRASRLENDFKVAGSDGYAVKGKYRTHGVGVSLEAGRRFAHA 789

Qy        878 NDWFAEPQAEVMLWRTSGKRYRASNGLRVKVDANTATLGRLGLRFGRRIALAGGNIVQPY 937
              : || |||||: ::|  |  |||:|||||: :  :: ||||||  |:|| ||||  ||||
Db        790 DGWFLEPQAELAVFRVGGGAYRAANGLRVRDEGGSSVLGRLGLEVGKRIELAGGRQVQPY 849

Qy        938 ARLGWTQEFKSTGDVRTNGIGHAGAGRHGRVELGAGVDAALGKGHNLYASYEYAAGDRIN 997
               :    |||   | |||||| |    |  | ||| |: ||||:||:|||||||: | ::
Db        850 IKASVLQEFDGAGTVRTNGIAHRTELRGTRAELGLGMAAALGRGHSLYASYEYSKGPKLA 909

Qy        998 IPWSFHAGYRYSF 1010
              :||:||||||||:
Db        910 MPWTFHAGYRYSW 922
```

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RESULT 11
AAE16185
ID   AAE16185 standard; protein; 922 AA.
XX
AC   AAE16185;
XX
DT   15-JUN-2007  (revised)
DT   26-MAR-2002  (first entry)
XX
DE   Bordetella parapertussis pertactin outer membrane protein, p.70.
XX
KW   Pertactin; PRN; outer membrane protein; vaccine; Bordetella infection;
KW   therapy; antibiotic; antibacterial; p.70; BOND_PC; pertactin precursor;
KW   pertactin precursor [Bordetella parapertussis 12822]; prn; pertactin;
KW   pertactin [Bordetella parapertussis];
KW   pertactin precursor [Bordetella parapertussis]; GO5515; GO7155; GO9405;
KW   GO16020; GO19867
```

KW GO16020; GO19867.
XX
OS Bordetella parapertussis.
XX
FH Key   Location/Qualifiers
FT Region   254. .304
FT   /note= "Pertactin region I"
FT Region   564. .621
FT   /note= "Pertactin region II"
XX
PN WO200190143-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-EP006457.
XX
PR 25-MAY-2000; 2000US-0206969P.
XX
PA (INSP) INST PASTEUR.
XX
PI Guiso-Maclouf N, Boursaux-Eude C;
XX
DR WPI; 2002-097639/13.
DR N-PSDB; AAD26442.
DR PC:NCBI; gi129828.
DR PC:SWISSPROT; P24328.
XX
PT Polypeptides containing polymorphisms of the repeated regions of
PT pertactin in Bordetella species, useful in immunogenic compositions for
PT treating infections caused by Bordetella and in diagnostic methods.
XX
PS Disclosure; Page 34; 47pp; English.
XX
CC The present invention relates to Bordetella bronchiseptica pertactin

CC The present invention relates to Bordetella bronchiseptica pertactin
CC (outer membrane protein) or their fragments. Pertactin (PRN) is used as
CC vaccine. Pertactin antibody is useful for treating Bordetella infections
CC and used to detect Bordetella antigens in biological preparations or in
CC purifying corresponding proteins, glycoproteins or their mixtures when
CC used in affinity chromatographic columns. Pertactin is useful as antigens
CC to identify antibodies to Bordetella in materials such as human or other
CC animal tissue and human or other animal cells, as well as biological
CC fluids, such as human or other animal body fluids, including human sera,
CC and to determine the concentration of Ab in those materials. Thus the
CC antigens can be used for qualitative or quantitative determination of
CC Bordetella in a material. The present sequence is B. parapertussis
CC pertactin outer membrane protein, p.70
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 922 AA;

Query Match 24.7%; Score 1280; DB 5; Length 922;
Best Local Similarity 35.9%; Pred. No. 2e-67;
Matches 328; Conservative 118; Mismatches 301; Indels 166; Gaps 23;

```
Qy        247 GAPLAAHPPLDRVAAVHAGQ----------DGKVTLREVALRAHGPQATGVYAYMPGS 294
              ||  ||:   :  : : ||:             |  |     ::  | || ||    | :
Db         27 GAAPAAYADWNNQSIIKAGERQHGIHIKQSDGAGVRTATGTTIKVSGRQAQGVLLENPAA 86

Qy        295 EITLQGGTVSVQG---DDGAGVVAGAGLLDALPPGGTVRLDGTTVS--TDGANTD--AVL 347
              |:  | |:|:  |   |:|     |   : |    | :  |  |::  :|  : |  |:
Db         87 ELRFQNGSVTSSGQLFDEGVRRFLGTVTVKA----GKLVADHATLANVSDTRDDDGIALY 142

Qy        348 VRGDAARAEVVNTVLRTAKSLAAGVSAQHGGRVTLRQTRIETAGAGAEGISVLGFE---- 403
              | |: |:| : :: |:     | ||  : |  ||:::: |   |     :  |  |
Db        143 VAGTQAQAIADSTLQG---AGGVRVTRGANVTVQDSTIVDGGLHIGTLQPLQPEPLPP 198
```

```
Db        143 VAGEQAQASIADSTLQG----AGGVRVERGANVTVQRSTIVDGGLHIGTLQPLQPEDLPP 198

Qy        404 -------------PQSGSGPASVDMQGGSITT------TGNRAAGIALTHGS-ARLEGVA 443
                          | ||: ||:| : | :  |       || ||||:|   |:   |:
Db        199 SRVVLGDTSVTAVPASGA-PAAVFVFGANELTVDGGHITGGRAAGVAAMDGAIVHLQRAT 257

Qy        444 VR---AEGSGS-----------------------------------------SAAQLA---- 457
              :|   |   |:                                           | ||
Db        258 IRRGDAPAGGAVPGGAVPGGAVPGGFGPLLDGWYGVDVSDSTVDLAQSIVEAPQLGAAIR 317

Qy        458 ---NGTLVVSAGSLASAQSGAISVTDTPLKLMPGALASSTVSVRLTDGATAQGGNGVFLQ 514
                   : || |||::     |       :  | |   | :|: |  || |||     |
Db        318 AGRGARVTVSGGSLSAPHGNVIETGGGARRFPPPA---SPLSITLQAGARAQG--RALLY 372

Qy        515 QHSTIPVAVALESGALARGDIVADGNKPLDAG----ISLSVASGAAWHGATQVLQSATLG 570
              :    || : |  ||  :|||||    |:       : :::|| | | |||: : | ::
Db        373 RVLPEPVKLTLAGGAQGQGDIVATELPPIPGASSGPLDVALASQARWTGATRAVDSLSI- 431

Qy        571 KGGTWVVNADSRVQDMSMRG-GRVEFQAPAPEASYKTLTLQTLDGNGVFVLNTNVAAGQN 629
                 |||:  :| |  : :   | |:|| ||    :| | : || |:|:| :|     | :
Db        432 DNATWVMTDNSNVGALRLASDGSVDFQQPAEAGRFKVLMVDTLAGSGLFRMNVFADLGLS 491

Qy        630 DQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTQGQGNATFRLANVGKAVDLGTWRY 689
              |:| |   | ||||: |||:| |  | |  : || |     ||| |||    ||:||:||
Db        492 DKLVVMRDASGQHRLWVRNSGSEPAS-GNTMLLVQTPRGSAATFTLANKDGKVDIGTYRY 550

Qy        690 SLAEDPKTHVWSL-----------------------------------------QR------ 704
               || :     |||                                        ||
Db        551 RLAANGNGQ-WSLVGAKAPPAPKPAPQPGPQPGPQPPQPPQPPQPPQPPQPPQRQPEAPA 609

Qy        705 ----AGQALSGAANAAVNAADL---SSIALAESNALDKRLGELRLRADAGGPWARTFSER 757
                  ||: || |||||||   :   |::  |||||| ||||||||  |||| | | |::|
Db        610 PQPPAGRELSAAANAAVNTGGVGLASTLWYAESNALSKRLGELRLNPDAGGAWGRGFAQR 669
```

```
Qy         758 QQISNRHARAYDQTVSGLEIGLDRGWSASGGRWYAGGLLGYTYADRTYPGDGGGKVKGLH 817
               ||: ||  | :|| |:| |:| |   : :||||: ||| |||  || : |||||    :|
Db         670 QQLDNRAGRRFDQKVAGFELGADHAVAVAGGRWHLGGLAGYTRGDRGFTGDGGGHTDSVH 729

Qy         818 VGGYAAYVGDGGYYLDTVLRLGRYDQQYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELP 877
               ||||| |: : |:|||  ||  | :  : :||:||  |   ||| |   ||| ||||
Db         730 VGGYATYIANSGFYLDATLRASRLENDFKVAGSDGYAVKGKYRTHGVGVSLEAGRRFAHA 789

Qy         878 NDWFAEPQAEVMLWRTSGKRYRASNGLRVKVDANTATLGRLGLRFGRRIALAGGNIVQPY 937
               : || |||||: ::|  |  |||:|||||: :  :: ||||||  |:|| ||||  ||||
Db         790 DGWFLEPQAELAVFRVGGGAYRAANGLRVRDEGGSSVLGRLGLEVGKRIELAGGRQVQPY 849

Qy         938 ARLGWTQEFKSTGDVRTNGIGHAGAGRHGRVELGAGVDAALGKGHNLYASYEYAAGDRIN 997
                :    |||   | |||||| |    |  | ||| |: ||||:||:|||||||: | ::
Db         850 IKASVLQEFDGAGTVRTNGIAHRTELRGTRAELGLGMAAALGRGHSLYASYEYSKGPKLA 909

Qy         998 IPWSFHAGYRYSF 1010
               :||:||||||||:
Db         910 MPWTFHAGYRYSW 922


RESULT 12
AAR26503
ID   AAR26503 standard; protein; 911 AA.
XX
AC   AAR26503;
XX
DT   27-AUG-2003  (revised)
DT   25-MAR-2003  (revised)
DT   12-MAR-1993  (first entry)
XX
DE   prn proteins.
XX
```

XX
KW B. bronchiseptica; P.68; outer membrane protein; piglet; probe;
KW atrophic rhinitis; alternative cleavage.
XX
OS Bordetella bronchiseptica.
XX
FH Key Location/Qualifiers
FT Protein 35. .632
FT /label= P.68
FT Peptide 260. .262
FT /label= RGD_tripeptide
FT Region 266. .279
FT /label= Repeat_region
FT Region 570. .589
FT /label= Repeat_region
FT Peptide 701. .703
FT /label= RGD_tripeptide
XX
PN WO9217587-A1.
XX
PD 15-OCT-1992.
XX
PF 27-MAR-1992; 92WO-GB000561.
XX
PR 27-MAR-1991; 91GB-00006568.
XX
PA (WELL) WELLCOME FOUND LTD.
XX
PI Charles IG;
XX
DR WPI; 1992-366258/44.
DR N-PSDB; AAQ34566.
XX
DT DNA encoding a Bordetella bronchiseptica protein - used for obtaining

PT DNA encoding a Bordetella bronchiseptica protein - used for obtaining
PT vaccines for preventing respiratory diseases, partic. atrophic rhinitis
PT in pigs.
XX
PS Claim 1; Fig 1; 28pp; English.
XX
CC The sequence given is the P.94 antigen from B. bronchiseptica. The P.68
CC antigen is formed by alternative cleavage of this protein. P.68 is an
CC outer membrane protein with a molecular weight of 68 kD which is
CC associated with protection of piglets against atrophic rhinitis. The DNA
CC sequence encoding these proteins was derived by standard recombinant DNA
CC techniques using P.68 probes to isolate the entire P.94 sequence.
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 911 AA;

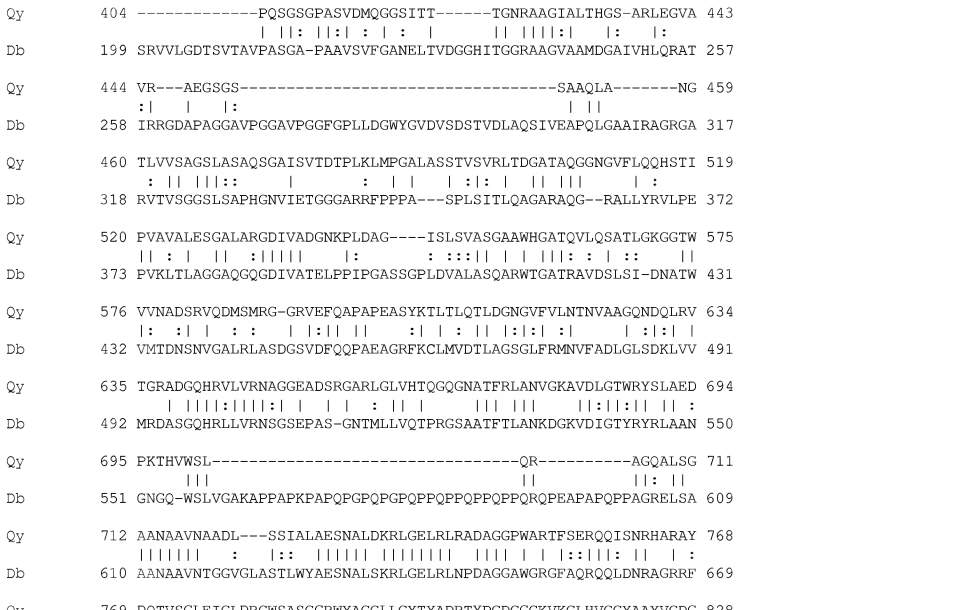
Query Match 24.6%; Score 1274.5; DB 2; Length 911;
Best Local Similarity 36.1%; Pred. No. 4.1e-67;
Matches 326; Conservative 119; Mismatches 302; Indels 155; Gaps 23;

```
Qy        247 GAPLAAHPPLDRVAAVHAGQ----------DGKVTLREVALRAHGPQATGVYAYMPGS 294
              ||  ||:   :  : : ||:             |  |     ::  | || ||    | :
Db         27 GAAPAAYADWNNQSIIKAGERQHGIHIKQSDGAGVRTATGTTIKVSGRQAQGVLLENPAA 86

Qy        295 EITLQGGTVSVQG---DDGAGVVAGAGLLDALPPGGTVRLDGTTVS--TDGANTD--AVL 347
              |:  | |:|:  |   |:|     |   : |    | :  |  |:::  :|  : |  |:
Db         87 ELRFQNGSVTSSGQLFDEGVRRFLGTVTVKA----GKLVADHATLANVSDTRDDDGIALY 142

Qy        348 VRGDAARAEVVNTVLRTAKSLAAGVSAQHGGRVTLRQTRIETAGAGAEGISVLGFE---- 403
              | |: |:| : :: |:     | ||  : |  ||:::: |   |     :  |  |
Db        143 VAGEQAQASIADSTLQG----AGGVRVERGANVTVQRSTIADGGLHIGTLQPLQPEDLPP 198

Qy        404                 DQSGGRASVDMQGGSITT       TGNDAAGIALTHGS APLEGVA 443
```



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              || |:| |:| |   : :|||| : ||| |||  || : |||||    ::|||| |: :
Db        670 DQKVAGFELGADHAVAVAGGRWHLGGLAGYTRGDRGFTGDGGGHTDNVNVGGYPTYIANS 729

Qy        829 GYYLDTVLRLGRYDQQYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQAEV 888
              |:|||  ||  | :  : :||:||  |   ||| |   ||| ||||   : || |||||:
Db        730 GFYLDATLRASRLENDFKVAGSDGYAVKGKYRTHGVGASLEAGRRFAHADGWFLEPQAEL 789

Qy        889 MLWRTSGKRYRASNGLRVKVDANTATLGRLGLRFGRRIALAGGNIVQPYARLGWTQEFKS 948
               ::|     |||:|||||: :  :: ||||||  |:|| ||||  |||| :    |||
Db        790 AVFRVGRGSYRAANGLRVRDEGGSSVLGRLGLEVGKRIELAGGRQVQPYIKASVLQEFDG 849

Qy        949 TGDVRTNGIGHAGAGRHGRVELGAGVDAALGKGHNLYASYEYAAGDRINIPWSFHAGYRY 1008
               | |||||| |    |  | ||| |: ||||:|||:|||||||: | :: :|||:|||||||
Db        850 AGTVRTNGIAHRTELRGTRAELGLGMAAALGRGHSLYASYEYSKGPKLAMPWTFHAGYRY 909

Qy       1009 SF 1010
              |:
Db        910 SW 911
```

```
RESULT 13
ABU23088
ID   ABU23088 standard; protein; 768 AA.
XX
AC   ABU23088;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Protein encoded by Prokaryotic essential gene #8615.
XX
KW   Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS   Bordetella pertussis.
XX
```

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003-029926/02.
DR N-PSDB; ACA26958.

XX

PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 51012; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the

CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 768 AA;

Query Match 23.9%; Score 1238.5; DB 6; Length 768;
Best Local Similarity 38.3%; Pred. No. 4.7e-65;
Matches 334; Conservative 95; Mismatches 281; Indels 163; Gaps 30;

Qy 195 AAQGGQASIIDATLQSILGPALIADGGSISVAGGSI---DMDMGPGFPPPPPPLPGAPLA 251

```
Db        378 ASANTLL-LVQTPLGSAATFTLANKDGKVDIGTYRYRLAANGNGQ-WSLVGAKAPPAPKP 435

Qy        703 ----------------------QRAGQALSGAANAAVNAADL---SSIALAESNALDKRL 737
                                     ||: || |||||||   :   |::  |||||| |||
Db        436 APQPGPQPPQPPQPQPEAPAPQPPAGRELSAAANAAVNTGGVGLASTLWYAESNALSKRL 495

Qy        738 GELRLRADAGGPWARTFSERQQISNRHARAYDQTVSGLEIGLDRGWSASGGRWYAGGLLG 797
              |||||  |||| | | |::|||: ||  | :|| |:| |:| |   : :||||: ||| |
Db        496 GELRLNPDAGGAWGRGFAQRQQLDNRAGRRFDQKVAGFELGADHAVAVAGGRWHLGGLAG 555

Qy        798 YTYADRTYPGDGGGKVKGLHVGGYAAYVGDGGYYLDTVLRLGRYDQQYNIAGTDGGRVTA 857
              ||  || : |||||    :|||||| |: | |:|||  ||  | :  : :|||:||  |
Db        556 YTRGDRGFTGDGGGHTDSVHVGGYATYIADSGFYLDATLRASRLENDFKVAGSDGYAVKG 615

Qy        858 DYRTSGAAWSLEGGRRFELPNDWFAEPQAEVMLWRTSGKRYRASNGLRVKVDANTATLGR 917
               ||| |   ||| ||||   : || |||||: ::|  |  |||:|||||: :  :: |||
Db        616 KYRTHGVGASLEAGRRFTHADGWFLEPQAELAVFRAGGGAYRAANGLRVRDEGGSSVLGR 675

Qy        918 LGLRFGRRIALAGGNIVQPYARLGWTQEFKSTGDVRTNGIGHAGAGRHGRVELGAGVDAA 977
              |||  |:|| ||||  |||| :    |||   | | |||| |    |  | ||| |: ||
Db        676 LGLEVGKRIELAGGRQVQPYIKASVLQEFDGAGTVHTNGIAHRTELRGTRAELGLGMAAA 735

Qy        978 LGKGHNLYASYEYAAGDRINIPWSFHAGYRYSF 1010
              ||:||:|||||||: | :: :||:||||||||:
Db        736 LGRGHSLYASYEYSKGPKLAMPWTFHAGYRYSW 768


RESULT 14
ADZ46890
ID   ADZ46890 standard; protein; 759 AA.
XX
AC   ADZ46890;
XX
DT   15-JUN-2007  (revised)
```

DT 15-JUN-2007 (revised)
DT 30-JUN-2005 (first entry)
XX
DE BASB232 polypeptide encoded by Orf22.
XX
KW BASB232; vaccine; bacterial infection; bordetella pertussis infection;
KW antibacterial; BOND_PC; putative autotransporter;
KW putative autotransporter [Bordetella pertussis]; BapC protein;
KW BapC protein [Bordetella pertussis Tohama I]; G05524; G07155.
XX
OS Bordetella pertussis.
XX
PN WO2005032584-A2.
XX
PD 14-APR-2005.
XX
PF 01-OCT-2004; 2004WO-EP011082.
XX
PR 02-OCT-2003; 2003GB-00023112.
PR 02-OCT-2003; 2003GB-00023113.
XX
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
XX
PI Castado C, Denoel P, Godfroid F, Poolman J;
XX
DR WPI; 2005-296056/30.
DR N-PSDB; ADZ46889.
DR PC:NCBI; gi3411270.
XX
PT Immunogenic composition, comprises polypeptide of Bordetella pertussis or
PT mixture of different B.pertussis, antigens, useful in Bordetella disease
PT treatments.
XX
PS Claim 3; SEQ ID NO 44; 172pp; English

PS Claim 3; SEQ ID NO 44; 172pp; English.
XX
CC The invention relates to BASB232 polypeptides (SEQ Group 2), and the
CC polynucleotide sequences (SEQ Group 1) encoding them. The invention also
CC relates to an immunogenic composition, comprising a B. pertussis BASB232
CC polypeptide or a mixture of 2-9 or 10 different B. pertussis antigens,
CC chosen from Bordetella autotransporter protein, Bordetella iron
CC acquisition protein, Bordetella lipoprotein, Bordetella adhesin and
CC Bordetella toxin/invasin, and an excipient. Also described is a vaccine
CC comprising the above immunogenic composition. The immunogenic composition
CC is useful in the preparation of a medicament for use in the treatment or
CC prevention of Bordetella disease such as whooping cough. The immunogenic
CC composition and vaccine are useful for treating or preventing Bordetella
CC infections such as B. pertussis, B. parapertussis or B. bronchiseptica
CC infections, by administering the vaccine to a host. This sequence
CC represents a BASB232 polypeptide of the invention.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 759 AA;

Query Match 23.0%; Score 1192.5; DB 10; Length 759;
Best Local Similarity 37.3%; Pred. No. 2.5e-62;
Matches 286; Conservative 99; Mismatches 277; Indels 105; Gaps 19;

```
Qy        328 TVRLDGTTVSTD-GANTDAVLVRGDAARAEVVNTVLRTAKSLAAGVSAQ---HGGRVTLR 383
              ::|: |  |    |||  ||:  | : :  : |  |  |  : |   ||    |||:
Db         14 SIRVQGGVVQGGMGANNVAVVATG-SGKVAIENAELLGASGMYATFGAQVDMKGGRILAH 72

Qy        384 QTRIETAGAGAEGISVLGFEPQSG---SGPASVDMQGGSITTTGNRAAGIAL-----THG 435
               | |  :   |:|       |  |   :    |:::|  :: ||  |||: |     |
Db         73 NTNILGSQGYADG-------PYGGVVVTEDGQVNLEGAKVSATGLGAAGLWLLGDKDTSP 125
```

```
Qy        436 SARLEGVAVRAEGSGSSAAQLA---NGTLVVSAGSLASAQSGAISVTDTP---------- 482
                | |    |  |      | :|   ||   :| ||| | : ||:  | ||
Db        126 RASLRNTDVHGE-----VAAIALGFNGEANISGGSL-SVEDGAVLTTLTPDAVEYYYDYA 179

Qy        483 --LKLMPGALASSTVSVRLTDGATAQGGNGVFLQQHSTIPVAVALESGALARGDIV---- 536
                :: :|     : | | |:||| | |     :     :|: : | ||  ||||||
Db        180 LSMEHLPADAPLTPVRVTLSDGARASG--ETLIAHGGLLPMTLRLSSGVDARGDIVTLPP 237

Qy        537 ----------------------------------------ADGNKPL----------DAGI 547
                                                       || :|:          || |
Db        238 SAPPDSAEQPDAEPEPDAELEPDAAAQSDAKANARVMAQVDGGEPVAVPIPAPSHPDAPI 297

Qy        548 SLSVASGAAWHGATQVLQSATLGKGGTWVVNADSRVQDMSMRGGRVEFQAPA-PEASYKT 606
                : : ||| | | |: : :  : : ||| |   | |  : :: |:| :  ||  :  :|
Db        298 DVFIDSGAQWRGMTKTVNALRI-EDGTWTVTGSSTVNSLHLQAGKVAYATPAESDGEFKH 356

Qy        607 LTLQTLDGNGVFVLNTNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTQ 666
                | ::|| |:|:| :| :      | | |:  | |||:|||| || |     : | ||
Db        357 LRVKTLSGSGLFEMNASADLSDGDLLVVSDEASGQHKVLVRGAGTEPTGVES-LTLVELP 415

Qy        667 GQGNATFRLANVGKAVDLGTWRYSLAEDPKTHVWSLQRAGQALSGAANAAVNAADL---S 723
                  | ||| |  || | :|| |   |   || |:|  | ||  ||||:|   :   |
Db        416 EGSQTKFTLANRGGVVDAGAFRYRLT--PDNGVWGLERTSQ-LSAVANAALNTGGVGAAS 472

Qy        724 SIALAESNALDKRLGELRLRADAGGPWARTFSERQQISNRHARAYDQTVSGLEIGLDRGW 783
                ||  || ||| |||||||   ||| | |||:::||: |:  | :|| | | |:| |
Db        473 SIWYAEGNALSKRLGELRLDPGAGGFWGRTFAQKQQLDNKAGRRFDQKVYGFELGADHAI 532

Qy        784 SASGGRWYAGGLLGYTYADRTYPGDGGGKVKGLHVGGYAAYVGDGGYYLDTVLRLGRYDQ 843
                :   |||: ||||||| | |::  || |     |:| ||||| | |:| |: ||  |::
Db        533 AGQQGRWHVGGLLGYTRARRSFIDDGAGHTDSAHIGAYAAYVADNGFYFDSTLRASRFEN 592

Qy        844 QYNLAGTDGGDVTADYRTSGAAWSLEGGRDFFLDNDWTAFDQAFVMLWDTGGKDYRASNG 903
```

```
Qy        844 QYNIAGTDGGRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQAEVMLWRTSGKRYRASNG 903
              : :  ||   |   || :|   :|| |:|| | : || |||:|| |:  ||  |||:|
Db        593 DFTVTATDAVSVRGKYRANGVGATLEAGKRFTLHDGWFVEPQSEVSLFHASGGTYRAANN 652

Qy        904 LRVKVDANTATLGRLGLRFGRRIALAGGNIVQPYARLGWTQEFKSTGDVRTNGIGHAGAG 963
              | || :  |: : ||||  |||| |    ::|||| | | ||||    ||||| |
Db        653 LSVKDEGGTSAVLRLGLAAGRRIDLGKDRVIQPYATLSWLQEFKGVTTVRTNGYGLRTDL 712

Qy        964 RHGRVELGAGVDAALGKGHNLYASYEYAAGDRINIPWSFHAGYRYSF 1010
                || ||  |: ||||:|| || ||||| |::: :||:|| ||||::
Db        713 SGGRAELALGLAAALGRGHQLYTSYEYAKGNKLTLPWTFHLGYRYTW 759


RESULT 15
ADZ46892
ID   ADZ46892 standard; protein; 515 AA.
XX
AC   ADZ46892;
XX
DT   30-JUN-2005  (first entry)
XX
DE   BASB232 polypeptide encoded by Orf23.
XX
KW   BASB232; vaccine; bacterial infection; bordetella pertussis infection;
KW   antibacterial.
XX
OS   Bordetella pertussis.
XX
PN   WO2005032584-A2.
XX
PD   14-APR-2005.
XX
PF   01-OCT-2004; 2004WO-EP011082.
XX
```

XX
PR 02-OCT-2003; 2003GB-00023112.
PR 02-OCT-2003; 2003GB-00023113.
XX
PA (GLAX) GLAXOSMITHKLINE BIOLOGICALS SA.
XX
PI Castado C, Denoel P, Godfroid F, Poolman J;
XX
DR WPI; 2005-296056/30.
DR N-PSDB; ADZ46891.
XX
PT Immunogenic composition, comprises polypeptide of Bordetella pertussis or
PT mixture of different B.pertussis, antigens, useful in Bordetella disease
PT treatments.
XX
PS Claim 3; SEQ ID NO 46; 172pp; English.
XX
CC The invention relates to BASB232 polypeptides (SEQ Group 2), and the
CC polynucleotide sequences (SEQ Group 1) encoding them. The invention also
CC relates to an immunogenic composition, comprising a B. pertussis BASB232
CC polypeptide or a mixture of 2-9 or 10 different B. pertussis antigens,
CC chosen from Bordetella autotransporter protein, Bordetella iron
CC acquisition protein, Bordetella lipoprotein, Bordetella adhesin and
CC Bordetella toxin/invasin, and an excipient. Also described is a vaccine
CC comprising the above immunogenic composition. The immunogenic composition
CC is useful in the preparation of a medicament for use in the treatment or
CC prevention of Bordetella disease such as whooping cough. The immunogenic
CC composition and vaccine are useful for treating or preventing Bordetella
CC infections such as B. pertussis, B. parapertussis or B. bronchiseptica
CC infections, by administering the vaccine to a host. This sequence
CC represents a BASB232 polypeptide of the invention.
XX
SQ Sequence 515 AA;

```
  Query Match             21.7%;  Score 1122.5;  DB 10;  Length 515;
  Best Local Similarity   45.7%;  Pred. No. 2.3e-58;
  Matches  237;  Conservative   65;  Mismatches  192;  Indels   25;  Gaps    7;

Qy        513 LQQHSTIPVAVALESGALARGDIV--------ADG-NKPLDAG---------ISLSVASG 554
              |:| : :|| : |   |:|:|||:|          ||   |:  |          : | || |
Db          1 LRQTTPVPVRLVLRGAAVAQGDVVRAPETAPEKDGFGTPVRPGLRVGLDQAPLELDVADG 60

Qy        555 AAWHGATQVLQSATLGKGGTWVVNADSRVQDMSMRGGRVEFQAPAPEASYKTLTLQTLDG 614
              | |||||| |    || || | ::| | | ::||  |        |    ::|||::|| |
Db         61 AQWHGATQSLDRLALGAGGQWRMSAASSVGELSMEPGAAVVFGDAAGPGFQTLTVRTLAG 120

Qy        615 NGVFVLNTNVAAGQNDQLRVTGRADGQHRVLVRNAGGEADSRGARLGLVHTQGQGNATFR 674
               | | :  : |    ||| || :|:|:||| :|   |   |: |:  ||     | |:|
Db        121 AGSFEMRADAALEHADQLVVTDQAEGRHRVWLRAPAGAEPSK-AQAVLVRAPADGKASFE 179

Qy        675 LANVGKAVDLGTWRYSLAEDPKTHVWSLQRAGQALSGAANAAVNAADLSSIA---LAESN 731
              |       | ||:|| ||: |    | | | |   |  | ||::   | ::     ||||
Db        180 LDGSDGRADFGTYRYGLAQQP-GGAWGLVRTG--YSSTAAAALDTGGLGAVQGLWYAESN 236

Qy        732 ALDKRLGELRLRADAGGPWARTFSERQQISNRHARAYDQTVSGLEIGLDRGWSASGGRWY 791
              || ||:|||||  |||| | | ||:||:|| |  | : | |||:|:| || |  :||||:
Db        237 ALGKRMGELRLNPDAGGAWGRAFSQRQRISPRAGRHFQQGVSGIELGADRAWPVAGGRWH 296

Qy        792 AGGLLGYTYADRTYPGDGGGKVKGLHVGGYAAYVGDGGYYLDTVLRLGRYDQQYNIAGTD 851
              || ||||| | | : | | |    :|||||| |:|  | | |  ||  |::  ::  |
Db        297 AGWLLGYTRASRGFSGQGKGHTDSVHVGGYATYIGANGVYADATLRASRFENSFDAPGWA 356

Qy        852 GGRVTADYRTSGAAWSLEGGRRFELPNDWFAEPQAEVMLWRTSGKRYRASNGLRVKVDAN 911
              |  |:  || :|   :|| |||  |   || |||||:  :|  |  | ||||||:: |
Db        357 GRTVSGSYRANGVGVTLEAGRRLALDRHWFVEPQAELAWFRAGGGTYTASNGLRIEDDGG 416

Qy        912 TATLGDLGLDFGDRIALAGGNIVQDVARLGWTQEFKGTGDVDTNGIGHAGADHGDVTLG 971
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Qy        912 TATLGRLGLRFGRRIALAGGNIVQPYARLGWTQEFKSTGDVRTNGIGHAGAGRHGRVELG 971
              |:   |:| : |||  | || :|||||:| | || |    |||||| |      ||||||
Db        417 TSLQARVGAQAGRRFDLRGGAVVQPYAQLSWVQELKGVSTVRTNGIAHRTDLGAGRVELG 476

Qy        972 AGVDAALGKGHNLYASYEYAAGDRINIPWSFHAGYRYSF 1010
               || ||||||||||||||| | |:::||:   |||::
Db        477 LGVAAALGKGHNLYASYEYAHGPRLSLPWTVQLGYRYAW 515


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Job time : 101.58 secs
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